

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Kohei MIYAZONO; Takeshe IMAMURA; Peter DEN DIJKE
- (ii) TITLE OF INVENTION: ISOLATED ALK-1 PROTEIN, NUCLEIC ACIDS ENCODING IT, AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 46
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
 - (B) STREET: 666 Fifth Avenue
 - (C) CITY: New York City
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10103
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
 - (B) COMPUTER: IBM PS/2
 - (C) OPERATING SYSTEM: PC-DOS
 - (D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/039,177
 - (B) FILING DATE: March 13, 1998
 - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/GB93/02367
 - (B) FILING DATE: November 17, 1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: GB 9224057.1
 - (B) FILING DATE: November 17, 1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: GB 9304677.9
 - (B) FILING DATE: March 8, 1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: GB 9304680.3
 - (B) FILING DATE: March 8, 1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 9311047.6
 - (B) FILING DATE: May 28, 1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 9313763.6
 - (B) FILING DATE: July 2, 1993



(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 9136099.2
(B) FILING DATE: August 3, 1993

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 321344.5
(B) FILING DATE: October 15, 1993

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Mary Anne Schofield
(B) REGISTRATION NUMBER: 36,669
(C) REFERENCE/DOCKET NUMBER: LUD 5539 CIP - JEL/MAS

(ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO: 1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1984 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 283..1791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA	60
AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC	120
GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT	180
CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GTTCCGCCGA	240
AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC	294
Met Thr Leu Gly	

TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG	342
Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln	
5 10 15 20	
GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT	390
Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys	
25 30 35	
GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA	438
Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr	
40 45 50	
GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC	486
Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly	
55 60 65	
TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC	534
Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe	
70 75 80	
GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC	582
Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser	
85 90 95 100	
CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT	630
Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp	
105 110 115	
GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG	678
Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu	
120 125 130	
GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA CGG AGG CAG GAG	726
Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg Arg Arg Gln Glu	
135 140 145	
AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG	774
Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu	
150 155 160	
AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT	822
Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser	
165 170 175 180	
GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG	870
Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg	
185 190 195	
ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC	918
Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly Lys Gly Arg	
200 205 210	
TAT GGC GAA GTG TGG CGG GGC TTG TGG CAC GGT GAG AGT GTG GCC GTC	966
Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu Ser Val Ala Val	

215	220	225	
AAG ATC TTC TCC TCG AGG GAT GAA CAG TCC TGG TTC CGG GAG ACT GAG Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg Glu Thr Glu 230 235 240			1014
ATC TAT AAC ACA GTA TTG CTC AGA CAC GAC AAC ATC CTA GGC TTC ATC Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu Gly Phe Ile 245 250 255 260			1062
GCC TCA GAC ATG ACC TCC CGC AAC TCG AGC ACG CAG CTG TGG CTC ATC Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu Trp Leu Ile 265 270 275			1110
ACG CAC TAC CAC GAG CAC GGC TCC CTC TAC GAC TTT CTG CAG AGA CAG Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln Arg Gln 280 285 290			1158
ACG CTG GAG CCC CAT CTG GCT CTG AGG CTA GCT GTG TCC GCG GCA TGC Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val Ser Ala Ala Cys 295 300 305			1206
GGC CTG GCG CAC CTG CAC GTG GAG ATC TTC GGT ACA CAG GGC AAA CCA Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly Lys Pro 310 315 320			1254
GCC ATT GCC CAC CGC GAC TTC AAG AGC CGC AAT GTG CTG GTC AAG AGC Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val Lys Ser 325 330 335 340			1302
AAC CTG CAG TGT TGC ATC GCC GAC CTG GGC CTG GCT GTG ATG CAC TCA Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met His Ser 345 350 355			1350
CAG GGC AGC GAT TAC CTG GAC ATC GGC AAC AAC CCG AGA GTG GGC ACC Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr 360 365 370			1398
AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG ATC CGC ACG GAC Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp 375 380 385			1446
TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val 390 395 400			1494
CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp 405 410 415 420			1542
TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu 425 430 435			1590

GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT	1638
Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro	
440 445 450	
AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG	1686
Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met	
455 460 465	
CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG	1734
Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg	
470 475 480	
ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA	1782
Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys	
485 490 495 500	
GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC	1831
Val Ile Gln	
TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG	1891
TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCCACCC AGCCAAAAAT	1951
ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA	1984

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala	
1 5 10 15	
Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val	
20 25 30	
Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly	
35 40 45	
Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln	
50 55 60	
Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg	
65 70 75 80	
Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn	
85 90 95	
His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln	
100 105 110	
Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala	
115 120 125	
Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg	
130 135 140	

Arg	Arg	Gln	Glu	Lys	Gln	Arg	Gly	Leu	His	Ser	Glu	Leu	Gly	Glu	Ser	145	150	155	160
Ser	Leu	Ile	Leu	Lys	Ala	Ser	Glu	Gln	Gly	Asp	Thr	Met	Leu	Gly	Asp	165	170	175	
Leu	Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	180	185	190	
Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	195	200	205	
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Leu	Trp	His	Gly	Glu	210	215	220	
Ser	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	225	230	235	240
Arg	Glu	Thr	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	245	250	255	
Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	260	265	270	
Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	275	280	285	
Leu	Gln	Arg	Gln	Thr	Leu	Glu	Pro	His	Leu	Ala	Leu	Arg	Leu	Ala	Val	290	295	300	
Ser	Ala	Ala	Cys	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	305	310	315	320
Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Phe	Lys	Ser	Arg	Asn	Val	325	330	335	
Leu	Val	Lys	Ser	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	340	345	350	
Val	Met	His	Ser	Gln	Gly	Ser	Asp	Tyr	Leu	Asp	Ile	Gly	Asn	Asn	Pro	355	360	365	
Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Gln	370	375	380	
Ile	Arg	Thr	Asp	Cys	Phe	Glu	Ser	Tyr	Lys	Trp	Thr	Asp	Ile	Trp	Ala	385	390	395	400
Phe	Gly	Leu	Val	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Thr	Ile	Val	Asn	Gly	405	410	415	
Ile	Val	Glu	Asp	Tyr	Arg	Pro	Pro	Phe	Tyr	Asp	Val	Val	Pro	Asn	Asp	420	425	430	
Pro	Ser	Phe	Glu	Asp	Met	Lys	Lys	Val	Val	Cys	Val	Asp	Gln	Gln	Thr	435	440	445	
Pro	Thr	Ile	Pro	Asn	Arg	Leu	Ala	Ala	Asp	Pro	Val	Leu	Ser	Gly	Leu	450	455	460	
Ala	Gln	Met	Met	Arg	Glu	Cys	Trp	Tyr	Pro	Asn	Pro	Ser	Ala	Arg	Leu	465	470	475	480
Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Gln	Lys	Ile	Ser	Asn	Ser	Pro	485	490	495	
Glu	Lys	Pro	Lys	Val	Ile	Gln										500			

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 104..1630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCCGAGTAC CCCAGTGACC AGAGTGAGAG AAGCTCTGAA CGAGGGCACG CGGCTTGAAG	60
GACTGTGGGC AGATGTGACC AAGAGCCTGC ATTAAGTTGT ACA ATG GTA GAT GGA	115
Met Val Asp Gly	
1	
GTG ATG ATT CTT CCT GTG CTT ATC ATG ATT GCT CTC CCC TCC CCT AGT	163
Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu Pro Ser Pro Ser	
5 10 15 20	
ATG GAA GAT GAG AAG CCC AAG GTC AAC CCC AAA CTC TAC ATG TGT GTG	211
Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu Tyr Met Cys Val	
25 30 35	
TGT GAA GGT CTC TCC TGC GGT AAT GAG GAC CAC TGT GAA GGC CAG CAG	259
Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu Gly Gln Gln	
40 45 50	
TGC TTT TCC TCA CTG AGC ATC AAC GAT GGC TTC CAC GTC TAC CAG AAA	307
Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His Val Tyr Gln Lys	
55 60 65	
GGC TGC TTC CAG GTT TAT GAG CAG GGA AAG ATG ACC TGT AAG ACC CCG	355
Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr Cys Lys Thr Pro	
70 75 80	
CCG TCC CCT GGC CAA GCT GTG GAG TGC TGC CAA GGG GAC TGG TGT AAC	403
Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly Asp Trp Cys Asn	
85 90 95 100	
AGG AAC ATC ACG GCC CAG CTG CCC ACT AAA GGA AAA TCC TTC CCT GGA	451
Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys Ser Phe Pro Gly	
105 110 115	
ACA CAG AAT TTC CAC TTG GAG GTT GGC CTC ATT ATT CTC TCT GTA GTG	499
Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile Leu Ser Val Val	
120 125 130	

TTC GCA GTA TGT CTT TTA GCC TGC CTG CTG GGA GTT GCT CTC CGA AAA	547
Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val Ala Leu Arg Lys	
135 140 145	
TTT AAA AGG CGC AAC CAA GAA CGC CTC AAT CCC CGA GAC GTG GAG TAT	595
Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg Asp Val Glu Tyr	
150 155 160	
GGC ACT ATC GAA GGG CTC ATC ACC ACC AAT GTT GGA GAC AGC ACT TTA	643
Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly Asp Ser Thr Leu	
165 170 175 180	
GCA GAT TTA TTG GAT CAT TCG TGT ACA TCA GGA AGT GGC TCT GGT CTT	691
Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly Ser Gly Leu	
185 190 195	
CCT TTT CTG GTA CAA AGA ACA GTG GCT CGC CAG ATT ACA CTG TTG GAG	739
Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile Thr Leu Leu Glu	
200 205 210	
TGT GTC GGG AAA GGC AGG TAT GGT GAG GTG TGG AGG GGC AGC TGG CAA	787
Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp Gln	
215 220 225	
GGG GAA AAT GTT GCC GTG AAG ATC TTC TCC TCC CGT GAT GAG AAG TCA	835
Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Lys Ser	
230 235 240	
TGG TTC AGG GAA ACG GAA TTG TAC AAC ACT GTG ATG CTG AGG CAT GAA	883
Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met Leu Arg His Glu	
245 250 255 260	
AAT ATC TTA GGT TTC ATT GCT TCA GAC ATG ACA TCA AGA CAC TCC AGT	931
Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg His Ser Ser	
265 270 275	
ACC CAG CTG TGG TTA ATT ACA CAT TAT CAT GAA ATG GGA TCG TTG TAC	979
Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met Gly Ser Leu Tyr	
280 285 290	
GAC TAT CTT CAG CTT ACT ACT CTG GAT ACA GTT AGC TGC CTT CGA ATA	1027
Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser Cys Leu Arg Ile	
295 300 305	
GTG CTG TCC ATA GCT AGT GGT CTT GCA CAT TTG CAC ATA GAG ATA TTT	1075
Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His Ile Glu Ile Phe	
310 315 320	
GGG ACC CAA GGG AAA CCA GCC ATT GCC CAT CGA GAT TTA AAG AGC AAA	1123
Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys	
325 330 335 340	
AAT ATT CTG GTT AAG AAG AAT GGA CAG TGT TGC ATA GCA GAT TTG GGC	1171
Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile Ala Asp Leu Gly	

345	350	355	
CTG GCA GTC ATG CAT TCC CAG AGC ACC AAT CAG CTT GAT GTG GGG AAC			1219
Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu Asp Val Gly Asn			
360	365	370	
AAT CCC CGT GTG GGC ACC AAG CGC TAC ATG GCC CCC GAA GTT CTA GAT			1267
Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp			
375	380	385	
GAA ACC ATC CAG GTG GAT TGT TTC GAT TCT TAT AAA AGG GTC GAT ATT			1315
Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys Arg Val Asp Ile			
390	395	400	
TGG GCC TTT GGA CTT GTT TTG TGG GAA GTG GCC AGG CGG ATG GTG AGC			1363
Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg Arg Met Val Ser			
405	410	415	420
AAT GGT ATA GTG GAG GAT TAC AAG CCA CCG TTC TAC GAT GTG GTT CCC			1411
Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr Asp Val Val Pro			
425	430	435	
AAT GAC CCA AGT TTT GAA GAT ATG AGG AAG GTA GTC TGT GTG GAT CAA			1459
Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val Cys Val Asp Gln			
440	445	450	
CAA AGG CCA AAC ATA CCC AAC AGA TGG TTC TCA GAC CCG ACA TTA ACC			1507
Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp Pro Thr Leu Thr			
455	460	465	
TCT CTG GCC AAG CTA ATG AAA GAA TGC TGG TAT CAA AAT CCA TCC GCA			1555
Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln Asn Pro Ser Ala			
470	475	480	
AGA CTC ACA GCA CTG CGT ATC AAA AAG ACT TTG ACC AAA ATT GAT AAT			1603
Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys Ile Asp Asn			
485	490	495	500
TCC CTC GAC AAA TTG AAA ACT GAC TGT TGACATTTTC ATAGTGTCAA			1650
Ser Leu Asp Lys Leu Lys Thr Asp Cys			
505			
GAAGGAAGAT TTGACGTTGT TGTCATTGTC CAGCTGGGAC CTAATGCTGG CCTGACTGGT			1710
TGTCAGAATG GAATCCATCT GTCTCCCTCC CCAAATGGCT GCTTTGACAA GGCAGACGTC			1770
GTACCCAGCC ATGTGTTGGG GAGACATCAA AACCACCCTA ACCTCGCTCG ATGACTGTGA			1830
ACTGGGCATT TCACGAACTG TTCACACTGC AGAGACTAAT GTTGGACAGA CACTGTTGCA			1890
AAGGTAGGGA CTGGAGGAAC ACAGAGAAAT CCTAAAAGAG ATCTGGGCAT TAAGTCAGTG			1950
GCTTTGCATA GCTTTACAA GTCTCCTAGA CACTCCCCAC GGGAAACTCA AGGAGGTGGT			2010

GAATTTTAA TCAGCAATAT TGCCTGTGCT TCTCTTCTTT ATTGCACTAG GAATTCTTTG	2070
CATTCCTTAC TTGCACTGTT ACTCTTAATT TTAAAGACCC AACTTGCCAA AATGTTGGCT	2130
GCGTACTCCA CTGGTCTGTC TTTGGATAAT AGGAATTCAA TTTGGCAAAA CAAAATGTAA	2190
TGTCAGACTT TGCTGCATTT TACACATGTG CTGATGTTTA CAATGATGCC GAACATTAGG	2250
AATTGTTTAT ACACAACTTT GCAAATTATT TATTACTTGT GCACTTAGTA GTTTTTACAA	2310
AACTGCTTTG TGCATATGTT AAAGCTTATT TTTATGTGGT CTTATGATTT TATTACAGAA	2370
ATGTTTTTAA CACTATACTC TAAAATGGAC ATTTTCTTTT ATTATCAGTT AAAATCACAT	2430
TTTAAGTGCT TCACATTTGT ATGTGTGTAG ACTGTAACCT TTTTTCAGTT CATATGCAGA	2490
ACGTATTTAG CCATTACCCA CGTGACACCA CCGAATATAT TATCGATTTA GAAGCAAAGA	2550
TTTCAGTAGA ATTTTAGTCC TGAACGCTAC GGGGAAAATG CATTTTCTTC AGAATTATCC	2610
ATTACGTGCA TTAAACTCT GCCAGAAAAA AATAACTATT TTGTTTTAAT CTACTTTTTG	2670
TATTTAGTAG TTATTTGTAT AAATTAAATA AACTGTTTTT AAGTCAAAAA AAAA	2724

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Val	Asp	Gly	Val	Met	Ile	Leu	Pro	Val	Leu	Ile	Met	Ile	Ala	Leu
1				5				10						15	
Pro	Ser	Pro	Ser	Met	Glu	Asp	Glu	Lys	Pro	Lys	Val	Asn	Pro	Lys	Leu
			20					25						30	
Tyr	Met	Cys	Val	Cys	Glu	Gly	Leu	Ser	Cys	Gly	Asn	Glu	Asp	His	Cys
		35					40					45			
Glu	Gly	Gln	Gln	Cys	Phe	Ser	Ser	Leu	Ser	Ile	Asn	Asp	Gly	Phe	His
	50					55					60				
Val	Tyr	Gln	Lys	Gly	Cys	Phe	Gln	Val	Tyr	Glu	Gln	Gly	Lys	Met	Thr
	65				70				75					80	
Cys	Lys	Thr	Pro	Pro	Ser	Pro	Gly	Gln	Ala	Val	Glu	Cys	Cys	Gln	Gly
			85				90							95	
Asp	Trp	Cys	Asn	Arg	Asn	Ile	Thr	Ala	Gln	Leu	Pro	Thr	Lys	Gly	Lys
			100				105						110		
Ser	Phe	Pro	Gly	Thr	Gln	Asn	Phe	His	Leu	Glu	Val	Gly	Leu	Ile	Ile
		115					120					125			

Leu	Ser	Val	Val	Phe	Ala	Val	Cys	Leu	Leu	Ala	Cys	Leu	Leu	Gly	Val
130						135					140				
Ala	Leu	Arg	Lys	Phe	Lys	Arg	Arg	Asn	Gln	Glu	Arg	Leu	Asn	Pro	Arg
145					150					155					160
Asp	Val	Glu	Tyr	Gly	Thr	Ile	Glu	Gly	Leu	Ile	Thr	Thr	Asn	Val	Gly
				165					170					175	
Asp	Ser	Thr	Leu	Ala	Asp	Leu	Leu	Asp	His	Ser	Cys	Thr	Ser	Gly	Ser
			180					185					190		
Gly	Ser	Gly	Leu	Pro	Phe	Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Ile
		195					200					205			
Thr	Leu	Leu	Glu	Cys	Val	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg
	210					215					220				
Gly	Ser	Trp	Gln	Gly	Glu	Asn	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg
225				230						235					240
Asp	Glu	Lys	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Leu	Tyr	Asn	Thr	Val	Met
				245					250					255	
Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser
			260					265					270		
Arg	His	Ser	Ser	Thr	Gln	Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	Met
	275						280					285			
Gly	Ser	Leu	Tyr	Asp	Tyr	Leu	Gln	Leu	Thr	Thr	Leu	Asp	Thr	Val	Ser
	290					295					300				
Cys	Leu	Arg	Ile	Val	Leu	Ser	Ile	Ala	Ser	Gly	Leu	Ala	His	Leu	His
305				310						315					320
Ile	Glu	Ile	Phe	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp
				325					330					335	
Leu	Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Gln	Cys	Cys	Ile
			340					345					350		
Ala	Asp	Leu	Gly	Leu	Ala	Val	Met	His	Ser	Gln	Ser	Thr	Asn	Gln	Leu
	355						360					365			
Asp	Val	Gly	Asn	Asn	Pro	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro
	370					375					380				
Glu	Val	Leu	Asp	Glu	Thr	Ile	Gln	Val	Asp	Cys	Phe	Asp	Ser	Tyr	Lys
385				390						395					400
Arg	Val	Asp	Ile	Trp	Ala	Phe	Gly	Leu	Val	Leu	Trp	Glu	Val	Ala	Arg
				405					410					415	
Arg	Met	Val	Ser	Asn	Gly	Ile	Val	Glu	Asp	Tyr	Lys	Pro	Pro	Phe	Tyr
			420					425					430		
Asp	Val	Val	Pro	Asn	Asp	Pro	Ser	Phe	Glu	Asp	Met	Arg	Lys	Val	Val
	435						440					445			
Cys	Val	Asp	Gln	Gln	Arg	Pro	Asn	Ile	Pro	Asn	Arg	Trp	Phe	Ser	Asp
	450					455					460				
Pro	Thr	Leu	Thr	Ser	Leu	Ala	Lys	Leu	Met	Lys	Glu	Cys	Trp	Tyr	Gln
465					470					475					480
Asn	Pro	Ser	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Thr
				485					490					495	
Lys	Ile	Asp	Asn	Ser	Leu	Asp	Lys	Leu	Lys	Thr	Asp	Cys			
			500					505							

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2932 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 310..1905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCTCCGCGCC GAGGGCTGGA GGATGCGTTC CCTGGGGTCC GGACTTATGA AAATATGCAT	60
CAGTTTAATA CTGTCTTGGA ATTCATGAGA TGGAAGCATA GGTCAAAGCT GTTTGGAGAA	120
AATCAGAAGT ACAGTTTTAT CTAGCCACAT CTTGGAGGAG TCGTAAGAAA GCAGTGGGAG	180
TTGAAGTCAT TGTCAAGTGC TTGCGATCTT TTACAAGAAA ATCTCACTGA ATGATAGTCA	240
TTTAAATTGG TGAAGTAGCA AGACCAATTA TTAAAGGTGA CAGTACACAG GAAACATTAC	300
AATTGAACA ATG ACT CAG CTA TAC ATT TAC ATC AGA TTA TTG GGA GCC	348
Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala	
1 5 10	
TAT TTG TTC ATC ATT TCT CGT GTT CAA GGA CAG AAT CTG GAT AGT ATG	396
Tyr Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met	
15 20 25	
CTT CAT GGC ACT GGG ATG AAA TCA GAC TCC GAC CAG AAA AAG TCA GAA	444
Leu His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu	
30 35 40 45	
AAT GGA GTA ACC TTA GCA CCA GAG GAT ACC TTG CCT TTT TTA AAG TGC	492
Asn Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys	
50 55 60	
TAT TGC TCA GGG CAC TGT CCA GAT GAT GCT ATT AAT AAC ACA TGC ATA	540
Tyr Cys Ser Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile	
65 70 75	
ACT AAT GGA CAT TGC TTT GCC ATC ATA GAA GAA GAT GAC CAG GGA GAA	588
Thr Asn Gly His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu	
80 85 90	

ACC ACA TTA GCT TCA GGG TGT ATG AAA TAT GAA GGA TCT GAT TTT CAG	636
Thr Thr Leu Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln	
95 100 105	
TGC AAA GAT TCT CCA AAA GCC CAG CTA CGC CGG ACA ATA GAA TGT TGT	684
Cys Lys Asp Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys	
110 115 120 125	
CGG ACC AAT TTA TGT AAC CAG TAT TTG CAA CCC ACA CTG CCC CCT GTT	732
Arg Thr Asn Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val	
130 135 140	
GTC ATA GGT CCG TTT TTT GAT GGC AGC ATT CGA TGG CTG GTT TTG CTC	780
Val Ile Gly Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu	
145 150 155	
ATT TCT ATG GCT GTC TGC ATA ATT GCT ATG ATC ATC TTC TCC AGC TGC	828
Ile Ser Met Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys	
160 165 170	
TTT TGT TAC AAA CAT TAT TGC AAG AGC ATC TCA AGC AGA CGT CGT TAC	876
Phe Cys Tyr Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr	
175 180 185	
AAT CGT GAT TTG GAA CAG GAT GAA GCA TTT ATT CCA GTT GGA GAA TCA	924
Asn Arg Asp Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser	
190 195 200 205	
CTA AAA GAC CTT ATT GAC CAG TCA CAA AGT TCT GGT AGT GGG TCT GGA	972
Leu Lys Asp Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly	
210 215 220	
CTA CCT TTA TTG GTT CAG CGA ACT ATT GCC AAA CAG ATT CAG ATG GTC	1020
Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val	
225 230 235	
CGG CAA GTT GGT AAA GGC CGA TAT GGA GAA GTA TGG ATG GGC AAA TGG	1068
Arg Gln Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp	
240 245 250	
CGT GGC GAA AAA GTG GCG GTG AAA GTA TTC TTT ACC ACT GAA GAA GCC	1116
Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala	
255 260 265	
AGC TGG TTT CGA GAA ACA GAA ATC TAC CAA ACT GTG CTA ATG CGC CAT	1164
Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His	
270 275 280 285	
GAA AAC ATA CTT GGT TTC ATA GCG GCA GAC ATT AAA GGT ACA GGT TCC	1212
Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser	
290 295 300	
TGG ACT CAG CTC TAT TTG ATT ACT GAT TAC CAT GAA AAT GGA TCT CTC	1260
Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu	

465		470		475		480									
Pro	Ile	Val	Ser	Asn	Arg	Trp	Asn	Ser	Asp	Glu	Cys	Leu	Arg	Ala	Val
			485				490						495		
Leu	Lys	Leu	Met	Ser	Glu	Cys	Trp	Ala	His	Asn	Pro	Ala	Ser	Arg	Leu
		500					505						510		
Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ala	Lys	Met	Val	Glu	Ser	Gln
		515					520						525		
Asp	Val	Lys	Ile												
	530														

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT GTT GTC CTC	48
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu	
1 5 10 15	
CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG GTC CAG GCT CTG	96
Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Val Gln Ala Leu	
20 25 30	
CTG TGT GCG TGC ACC AGC TGC CTC CAG GCC AAC TAC ACG TGT GAG ACA	144
Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr	
35 40 45	
GAT GGG GCC TGC ATG GTT TCC TTT TTC AAT CTG GAT GGG ATG GAG CAC	192
Asp Gly Ala Cys Met Val Ser Phe Phe Asn Leu Asp Gly Met Glu His	
50 55 60	
CAT GTG CGC ACC TGC ATC CCC AAA GTG GAG CTG GTC CCT GCC GGG AAG	240
His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys	

305	310	315	
TAT GAC TTC CTG AAA TGT GCT ACA CTG GAC ACC AGA GCC CTG CTT AAA Tyr Asp Phe Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys 320 325 330			1308
TTG GCT TAT TCA GCT GCC TGT GGT CTG TGC CAC CTG CAC ACA GAA ATT Leu Ala Tyr Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile 335 340 345			1356
TAT GGC ACC CAA GGA AAG CCC GCA ATT GCT CAT CGA GAC CTA AAG AGC Tyr Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser 350 355 360 365			1404
AAA AAC ATC CTC ATC AAG AAA AAT GGG AGT TGC TGC ATT GCT GAC CTG Lys Asn Ile Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu 370 375 380			1452
GGC CTT GCT GTT AAA TTC AAC AGT GAC ACA AAT GAA GTT GAT GTG CCC Gly Leu Ala Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro 385 390 395			1500
TTG AAT ACC AGG GTG GGC ACC AAA CGC TAC ATG GCT CCC GAA GTG CTG Leu Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu 400 405 410			1548
GAC GAA AGC CTG AAC AAA AAC CAC TTC CAG CCC TAC ATC ATG GCT GAC Asp Glu Ser Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp 415 420 425			1596
ATC TAC AGC TTC GGC CTA ATC ATT TGG GAG ATG GCT CGT CGT TGT ATC Ile Tyr Ser Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile 430 435 440 445			1644
ACA GGA GGG ATC GTG GAA GAA TAC CAA TTG CCA TAT TAC AAC ATG GTA Thr Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val 450 455 460			1692
CCG AGT GAT CCG TCA TAC GAA GAT ATG CGT GAG GTT GTG TGT GTC AAA Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys 465 470 475			1740
CGT TTG CGG CCA ATT GTG TCT AAT CGG TGG AAC AGT GAT GAA TGT CTA Arg Leu Arg Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu 480 485 490			1788
CGA GCA GTT TTG AAG CTA ATG TCA GAA TGC TGG GCC CAC AAT CCA GCC Arg Ala Val Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala 495 500 505			1836
TCC AGA CTC ACA GCA TTG AGA ATT AAG AAG ACG CTT GCC AAG ATG GTT Ser Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val 510 515 520 525			1884

GAA TCC CAA GAT GTA AAA ATC TGATGGTTAA ACCATCGGAG GAGAAACTCT 1935
 Glu Ser Gln Asp Val Lys Ile
 530

AGACTGCAAG AACTGTTTTT ACCCATGGCA TGGGTGGAAT TAGAGTGGAA TAAGGATGTT 1995
 AACTTGGTTC TCAGACTCTT TCTTCACTAC GTGTTCACAG GCTGCTAATA TTAAACCTTT 2055
 CAGTACTCTT ATTAGGATAC AAGCTGGGAA CTTCTAAACA CTTCAATTCTT TATATATGGA 2115
 CAGCTTTATT TTAAATGTGG TTTTGTGATGC CTTTTTTTAA GTGGGTTTTT ATGAACTGCA 2175
 TCAAGACTTC AATCCTGATT AGTGTCTCCA GTCAAGCTCT GGGTACTGAA TTGCCTGTTC 2235
 ATAAAACGGT GCTTTCTGTG AAAGCCTTAA GAAGATAAAT GAGCGCAGCA GAGATGGAGA 2295
 AATAGACTTT GCCTTTTACC TGAGACATTC AGTTCGTTTG TATTCTACCT TTGTAAAACA 2355
 GCCTATAGAT GATGATGTGT TTGGGATACT GCTTATTTTA TGATAGTTTG TCCTGTGTCC 2415
 TTAGTGATGT GTGTGTGTCT CCATGCACAT GCACGCCGGG ATTCCTCTGC TGCCATTTGA 2475
 ATTAGAAGAA AATAATTTAT ATGCATGCAC AGGAAGATAT TGGTGGCCGG TGGTTTTGTG 2535
 CTTTAAAAAT GCAATATCTG ACCAAGATTC GCCAATCTCA TACAAGCCAT TTACTIONTGA 2595
 AGTGAGATAG CTTCCCCACC AGCTTTATTT TTTAACATGA AAGCTGATGC CAAGGCCAAA 2655
 AGAAGTTTAA AGCATCTGTA AATTTGGACT GTTTTCCTTC AACCACCATT TTTTTGTGG 2715
 TTATTATTTT TGTACGGAA AGCATCCTCT CCAAAGTTGG AGCTTCTATT GCCATGAACC 2775
 ATGCTTACAA AGAAAGCACT TCTTATTGAA GTGAATTCCT GCATTTGATA GCAATGTAAG 2835
 TGCCTATAAC CATGTTCTAT ATTCTTTATT CTCAGTAACT TTTAAAAGGG AAGTTATTTA 2895
 TATTTGTGT ATAATGTGCT TTATTGCAA ATCACCC 2932

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala Tyr Leu Phe
 1 5 10 15
 Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly
 20 25 30
 Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu Asn Gly Val

		35					40					45				
Thr	Leu	Ala	Pro	Glu	Asp	Thr	Leu	Pro	Phe	Leu	Lys	Cys	Tyr	Cys	Ser	
	50					55					60					
Gly	His	Cys	Pro	Asp	Asp	Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly	
65					70					75					80	
His	Cys	Phe	Ala	Ile	Ile	Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu	
				85				90						95		
Ala	Ser	Gly	Cys	Met	Lys	Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp	
			100					105					110			
Ser	Pro	Lys	Ala	Gln	Leu	Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn	
		115					120					125				
Leu	Cys	Asn	Gln	Tyr	Leu	Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly	
	130					135				140						
Pro	Phe	Phe	Asp	Gly	Ser	Ile	Arg	Trp	Leu	Val	Leu	Leu	Ile	Ser	Met	
145					150					155					160	
Ala	Val	Cys	Ile	Ile	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr	
				165					170					175		
Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Arg	Arg	Tyr	Asn	Arg	Asp	
			180					185					190			
Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp	
		195					200					205				
Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	
	210					215					220					
Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val	
225					230					235					240	
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu	
				245					250					255		
Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe	
			260					265					270			
Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile	
		275					280					285				
Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln	
	290					295					300					
Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe	
305					310					315					320	
Leu	Lys	Cys	Ala	Thr	Leu	Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	Ala	Tyr	
				325					330					335		
Ser	Ala	Ala	Cys	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Tyr	Gly	Thr	
			340					345					350			
Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile	
		355					360					365				
Leu	Ile	Lys	Lys	Asn	Gly	Ser	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	
	370					375					380					
Val	Lys	Phe	Asn	Ser	Asp	Thr	Asn	Glu	Val	Asp	Val	Pro	Leu	Asn	Thr	
385					390					395	</					

65	70	75	80	
CCC TTC TAC TGC CTG AGC TCG GAG GAC CTG CGC AAC ACC CAC TGC TGC				288
Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys	85	90	95	
TAC ACT GAC TAC TGC AAC AGG ATC GAC TTG AGG GTG CCC AGT GGT CAC				336
Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His	100	105	110	
CTC AAG GAG CCT GAG CAC CCG TCC ATG TGG GGC CCG GTG GAG CTG GTA				384
Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val	115	120	125	
GGC ATC ATC GCC GGC CCG GTG TTC CTC CTG TTC CTC ATC ATC ATC ATT				432
Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile	130	135	140	
GTT TTC CTT GTC ATT AAC TAT CAT CAG CGT GTC TAT CAC AAC CGC CAG				480
Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln	145	150	155	160
AGA CTG GAC ATG GAA GAT CCC TCA TGT GAG ATG TGT CTC TCC AAA GAC				528
Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp	165	170	175	
AAG ACG CTC CAG GAT CTT GTC TAC GAT CTC TCC ACC TCA GGG TCT GGC				576
Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly	180	185	190	
TCA GGG TTA CCC CTC TTT GTC CAG CGC ACA GTG GCC CGA ACC ATC GTT				624
Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val	195	200	205	
TTA CAA GAG ATT ATT GGC AAG GGT CGG TTT GGG GAA GTA TGG CGG GGC				672
Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly	210	215	220	
CGC TGG AGG GGT GGT GAT GTG GCT GTG AAA ATA TTC TCT TCT CGT GAA				720
Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu	225	230	235	240
GAA CGG TCT TGG TTC AGG GAA GCA GAG ATA TAC CAG ACG GTC ATG CTG				768
Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu	245	250	255	
CGC CAT GAA AAC ATC CTT GGA TTT ATT GCT GCT GAC AAT AAA GAT AAT				816
Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn	260	265	270	
GGC ACC TGG ACA CAG CTG TGG CTT GTT TCT GAC TAT CAT GAG CAC GGG				864
Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly	275	280	285	

TCC CTG TTT GAT TAT CTG AAC CGG TAC ACA GTG ACA ATT GAG GGG ATG	912
Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met	
290 295 300	
ATT AAG CTG GCC TTG TCT GCT GCT AGT GGG CTG GCA CAC CTG CAC ATG	960
Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met	
305 310 315 320	
GAG ATC GTG GGC ACC CAA GGG AAG CCT GGA ATT GCT CAT CGA GAC TTA	1008
Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu	
325 330 335	
AAG TCA AAG AAC ATT CTG GTG AAG AAA AAT GGC ATG TGT GCC ATA GCA	1056
Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala	
340 345 350	
GAC CTG GGC CTG GCT GTC CGT CAT GAT GCA GTC ACT GAC ACC ATT GAC	1104
Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp	
355 360 365	
ATT GCC CCG AAT CAG AGG GTG GGG ACC AAA CGA TAC ATG GCC CCT GAA	1152
Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu	
370 375 380	
GTA CTT GAT GAA ACC ATT AAT ATG AAA CAC TTT GAC TCC TTT AAA TGT	1200
Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys	
385 390 395 400	
GCT GAT ATT TAT GCC CTC GGG CTT GTA TAT TGG GAG ATT GCT CGA AGA	1248
Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg	
405 410 415	
TGC AAT TCT GGA GGA GTC CAT GAA GAA TAT CAG CTG CCA TAT TAC GAC	1296
Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp	
420 425 430	
TTA GTG CCC TCT GAC CCT TCC ATT GAG GAA ATG CGA AAG GTT GTA TGT	1344
Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys	
435 440 445	
GAT CAG AAG CTG CGT CCC AAC ATC CCC AAC TGG TGG CAG AGT TAT GAG	1392
Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu	
450 455 460	
GCA CTG CGG GTG ATG GGG AAG ATG ATG CGA GAG TGT TGG TAT GCC AAC	1440
Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn	
465 470 475 480	
GGC GCA GCC CGC CTG ACG GCC CTG CGC ATC AAG AAG ACC CTC TCC CAG	1488
Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln	
485 490 495	
CTC AGC GTG CAG GAA GAC GTG AAG ATC TAACTGCTCC CTCTCTCCAC	1535
Leu Ser Val Gln Glu Asp Val Lys Ile	

500

505

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ACGGAGCTCC TGGCAGCGAG AACTACGCAC AGCTGCCGCG TTGAGCGTAC GATGGAGGCC 1595
TACCTCTCGT TTCTGCCCAG CCCTCTGTGG CCAGGAGCCC TGGCCCGCAA GAGGGACAGA 1655
GCCCCGGGAGA GACTCGCTCA CTCCCATGTT GGGTTTGAGA CAGACACCTT TTCTATTTAC 1715
CTCCTAATGG CATGGAGACT CTGAGAGCGA ATTGTGTGGA GAACTCAGTG CCACACCTCG 1775
AACTGGTTGT AGTGGGAAGT CCCGCGAAAC CCGGTGCATC TGGCACGTGG CCAGGAGCCA 1835
TGACAGGGGC GCTTGGGAGG GGCCGGAGGA ACCGAGGTGT TGCCAGTGCT AAGCTGCCCT 1895
GAGGGTTTCC TTCGGGGACC AGCCACAGC ACACCAAGGT GGCCCGGAAG AACCAGAAGT 1955
GCAGCCCCCTC TCACAGGCAG CTCTGAGCCG CGCTTTCCCC TCCTCCCTGG GATGGACGCT 2015
GCCGGGAGAC TGCCAGTGGA GACGGAATCT GCCGCTTGT CTGTCCAGCC GTGTGTGCAT 2075
GTGCCGAGGT GCGTCCCCCG TTGTGCCTGG TTCGTGCCAT GCCCTTACAC GTGCGTGTGA 2135
GTGTGTGTGT GTGTCTGTAG GTGCGCACTT ACCTGCTTGA GCTTCTGTG CATGTGCAGG 2195
TCGGGGGTGT GGTTCGTCATG CTGTCCGTGC TTGCTGGTGC CTCTTTTCAG TAGTGAGCAG 2255
CATCTAGTTT CCCTGGTGCC CTTCCCTGGA GGTCTCTCCC TCCCCAGAG CCCCTCATGC 2315
CACAGTGGTA CTCTGTGT 2333

```

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu
 1             5             10             15
Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Val Gln Ala Leu
          20             25             30
Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr
          35             40             45
Asp Gly Ala Cys Met Val Ser Phe Phe Asn Leu Asp Gly Met Glu His
          50             55             60
His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys
          65             70             75             80
Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys
          85             90             95
Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His
          100             105             110

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Leu	Lys	Glu	Pro	Glu	His	Pro	Ser	Met	Trp	Gly	Pro	Val	Glu	Leu	Val	115	120	125
Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	Ile	Ile	Ile	130	135	140
Val	Phe	Leu	Val	Ile	Asn	Tyr	His	Gln	Arg	Val	Tyr	His	Asn	Arg	Gln	145	150	155
Arg	Leu	Asp	Met	Glu	Asp	Pro	Ser	Cys	Glu	Met	Cys	Leu	Ser	Lys	Asp	165	170	175
Lys	Thr	Leu	Gln	Asp	Leu	Val	Tyr	Asp	Leu	Ser	Thr	Ser	Gly	Ser	Gly	180	185	190
Ser	Gly	Leu	Pro	Leu	Phe	Val	Gln	Arg	Thr	Val	Ala	Arg	Thr	Ile	Val	195	200	205
Leu	Gln	Glu	Ile	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly	210	215	220
Arg	Trp	Arg	Gly	Gly	Asp	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu	225	230	235
Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu	245	250	255
Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn	260	265	270
Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly	275	280	285
Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Ile	Glu	Gly	Met	290	295	300
Ile	Lys	Leu	Ala	Leu	Ser	Ala	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met	305	310	315
Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Gly	Ile	Ala	His	Arg	Asp	Leu	325	330	335
Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Met	Cys	Ala	Ile	Ala	340	345	350
Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ala	Val	Thr	Asp	Thr	Ile	Asp	355	360	365
Ile	Ala	Pro	Asn	Gln	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	370	375	380
Val	Leu	Asp	Glu	Thr	Ile	Asn	Met	Lys	His	Phe	Asp	Ser	Phe	Lys	Cys	385	390	395
Ala	Asp	Ile	Tyr	Ala	Leu	Gly	Leu	Val	Tyr	Trp	Glu	Ile	Ala	Arg	Arg	405	410	415
Cys	Asn	Ser	Gly	Gly	Val	His	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asp	420	425	430
Leu	Val	Pro	Ser	Asp	Pro	Ser	Ile	Glu	Glu	Met	Arg	Lys	Val	Val	Cys	435	440	445
Asp	Gln	Lys	Leu	Arg	Pro	Asn	Ile	Pro	Asn	Trp	Trp	Gln	Ser	Tyr	Glu	450	455	460
Ala	Leu	Arg	Val	Met	Gly	Lys	Met	Met	Arg	Glu	Cys	Trp	Tyr	Ala	Asn	465	470	475
Gly	Ala	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ser	Gln	485	490	495
Leu	Ser	Val	Gln	Glu	Asp	Val	Lys	Ile								500	505	

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 77..1585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGCGAGGCGA GGTTCGCTGG GGTGAGGCAG CGGCGCGGCC GGGCCGGGCC GGGCCACAGG	60
CGGTGGCGGC GGGACC ATG GAG GCG GCG GTC GCT GCT CCG CGT CCC CGG	109
Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg	
1 5 10	
CTG CTC CTC CTC GTG CTG GCG GCG GCG GCG GCG GCG GCG GCG GCG CTG	157
Leu Leu Leu Leu Val Leu Ala Ala Ala Ala Ala Ala Ala Ala Ala Leu	
15 20 25	
CTC CCG GGG GCG ACG GCG TTA CAG TGT TTC TGC CAC CTC TGT ACA AAA	205
Leu Pro Gly Ala Thr Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys	
30 35 40	
GAC AAT TTT ACT TGT GTG ACA GAT GGG CTC TGC TTT GTC TCT GTC ACA	253
Asp Asn Phe Thr Cys Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr	
45 50 55	
GAG ACC ACA GAC AAA GTT ATA CAC AAC AGC ATG TGT ATA GCT GAA ATT	301
Glu Thr Thr Asp Lys Val Ile His Asn Ser Met Cys Ile Ala Glu Ile	
60 65 70 75	
GAC TTA ATT CCT CGA GAT AGG CCG TTT GTA TGT GCA CCC TCT TCA AAA	349
Asp Leu Ile Pro Arg Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys	
80 85 90	
ACT GGG TCT GTG ACT ACA ACA TAT TGC TGC AAT CAG GAC CAT TGC AAT	397
Thr Gly Ser Val Thr Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn	
95 100 105	
AAA ATA GAA CTT CCA ACT ACT GTA AAG TCA TCA CCT GGC CTT GGT CCT	445
Lys Ile Glu Leu Pro Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro	

110	115	120	
GTG GAA CTG GCA GCT GTC ATT GCT GGA CCA GTG TGC TTC GTC TGC ATC Val Glu Leu Ala Ala Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile 125 130 135			493
TCA CTC ATG TTG ATG GTC TAT ATC TGC CAC AAC CGC ACT GTC ATT CAC Ser Leu Met Leu Met Val Tyr Ile Cys His Asn Arg Thr Val Ile His 140 145 150 155			541
CAT CGA GTG CCA AAT GAA GAG GAC CCT TCA TTA GAT CGC CCT TTT ATT His Arg Val Pro Asn Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile 160 165 170			589
TCA GAG GGT ACT ACG TTG AAA GAC TTA ATT TAT GAT ATG ACA ACG TCA Ser Glu Gly Thr Thr Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser 175 180 185			637
GGT TCT GGC TCA GGT TTA CCA TTG CTT GTT CAG AGA ACA ATT GCG AGA Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg 190 195 200			685
ACT ATT GTG TTA CAA GAA AGC ATT GGC AAA GGT CGA TTT GGA GAA GTT Thr Ile Val Leu Gln Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val 205 210 215			733
TGG AGA GGA AAG TGG CGG GGA GAA GAA GTT GCT GTT AAG ATA TTC TCC Trp Arg Gly Lys Trp Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser 220 225 230 235			781
TCT AGA GAA GAA CGT TCG TGG TTC CGT GAG GCA GAG ATT TAT CAA ACT Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr 240 245 250			829
GTA ATG TTA CGT CAT GAA AAC ATC CTG GGA TTT ATA GCA GCA GAC AAT Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn 255 260 265			877
AAA GAC AAT GGT ACT TGG ACT CAG CTC TGG TTG GTG TCA GAT TAT CAT Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His 270 275 280			925
GAG CAT GGA TCC CTT TTT GAT TAC TTA AAC AGA TAC ACA GTT ACT GTG Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Val 285 290 295			973
GAA GGA ATG ATA AAA CTT GCT CTG TCC ACG GCG AGC GGT CTT GCC CAT Glu Gly Met Ile Lys Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala His 300 305 310 315			1021
CTT CAC ATG GAG ATT GTT GGT ACC CAA GGA AAG CCA GCC ATT GCT CAT Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His 320 325 330			1069

AGA GAT TTG AAA TCA AAG AAT ATC TTG GTA AAG AAG AAT GGA ACT TGC	1117
Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys	
335 340 345	
TGT ATT GCA GAC TTA GGA CTG GCA GTA AGA CAT GAT TCA GCC ACA GAT	1165
Cys Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ser Ala Thr Asp	
350 355 360	
ACC ATT GAT ATT GCT CCA AAC CAC AGA GTG GGA ACA AAA AGG TAC ATG	1213
Thr Ile Asp Ile Ala Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met	
365 370 375	
GCC CCT GAA GTT CTC GAT GAT TCC ATA AAT ATG AAA CAT TTT GAA TCC	1261
Ala Pro Glu Val Leu Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser	
380 385 390 395	
TTC AAA CGT GCT GAC ATC TAT GCA ATG GGC TTA GTA TTC TGG GAA ATT	1309
Phe Lys Arg Ala Asp Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile	
400 405 410	
GCT CGA CGA TGT TCC ATT GGT GGA ATT CAT GAA GAT TAC CAA CTG CCT	1357
Ala Arg Arg Cys Ser Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro	
415 420 425	
TAT TAT GAT CTT GTA CCT TCT GAC CCA TCA GTT GAA GAA ATG AGA AAA	1405
Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys	
430 435 440	
GTT GTT TGT GAA CAG AAG TTA AGG CCA AAT ATC CCA AAC AGA TGG CAG	1453
Val Val Cys Glu Gln Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln	
445 450 455	
AGC TGT GAA GCC TTG AGA GTA ATG GCT AAA ATT ATG AGA GAA TGT TGG	1501
Ser Cys Glu Ala Leu Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp	
460 465 470 475	
TAT GCC AAT GGA GCA GCT AGG CTT ACA GCA TTG CGG ATT AAG AAA ACA	1549
Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr	
480 485 490	
TTA TCG CAA CTC AGT CAA CAG GAA GGC ATC AAA ATG TAATTCTACA	1595
Leu Ser Gln Leu Ser Gln Gln Glu Gly Ile Lys Met	
495 500	
GCTTTGCCTG AACTCTCCTT TTTTCTTCAG ATCTGCTCCT GGGTTTTAAT TTGGGAGGTC	1655
AGTTGTTCTA CCTCACTGAG AGGGAACAGA AGGATATTGC TTCCTTTTGC AGCAGTGTA	1715
TAAAGTCAAT TAAAACTTC CCAGGATTTC TTTGGACCCA GGAAACAGCC ATGTGGGTCC	1775
TTTCTGTGCA CTATGAACGC TTCTTTCCCA GGACAGAAAA TGTGTAGTCT ACCTTTATTT	1835
TTTATTAACA AAACCTTGTTT TTAAAAAGA TGATTGCTGG TCTTAACTTT AGGTAACTCT	1895

GCTGTGCTGG AGATCATCTT TAAGGGCAAA GGAGTTGGAT TGCTGAATTA CAATGAAACA 1955
TGTCTTATTA CTAAAGAAAG TGATTTACTC CTGGTTAGTA CATTCTCAGA GGATTCTGAA 2015
CCACTAGAGT TTCCTTGATT CAGACTTTGA ATGTACTGTT CTATAGTTTT TCAGGATCTT 2075
AAAACATAACA CTTATAAAAC TCTTATCTTG AGTCTAAAAA TGACCTCATA TAGTAGTGAG 2135
GAACATAATT CATGCAATTG TATTTTGTAT ACTATTATTG TTCTTTCACT TATTCAGAAC 2195
ATTACATGCC TTCAAAATGG GATTGTACTA TACCAGTAAG TGCCACTTCT GTGTCTTTCT 2255
AATGGAAATG AGTAGAATTG CTGAAAGTCT CTATGTTAAA ACCTATAGTG TTT 2308

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met	Glu	Ala	Ala	Val	Ala	Ala	Pro	Arg	Pro	Arg	Leu	Leu	Leu	Leu	Val	1	5	10	15
Leu	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Leu	Leu	Pro	Gly	Ala	Thr	20	25	30	
Ala	Leu	Gln	Cys	Phe	Cys	His	Leu	Cys	Thr	Lys	Asp	Asn	Phe	Thr	Cys	35	40	45	
Val	Thr	Asp	Gly	Leu	Cys	Phe	Val	Ser	Val	Thr	Glu	Thr	Thr	Asp	Lys	50	55	60	
Val	Ile	His	Asn	Ser	Met	Cys	Ile	Ala	Glu	Ile	Asp	Leu	Ile	Pro	Arg	65	70	75	80
Asp	Arg	Pro	Phe	Val	Cys	Ala	Pro	Ser	Ser	Lys	Thr	Gly	Ser	Val	Thr	85	90	95	
Thr	Thr	Tyr	Cys	Cys	Asn	Gln	Asp	His	Cys	Asn	Lys	Ile	Glu	Leu	Pro	100	105	110	
Thr	Thr	Val	Lys	Ser	Ser	Pro	Gly	Leu	Gly	Pro	Val	Glu	Leu	Ala	Ala	115	120	125	
Val	Ile	Ala	Gly	Pro	Val	Cys	Phe	Val	Cys	Ile	Ser	Leu	Met	Leu	Met	130	135	140	
Val	Tyr	Ile	Cys	His	Asn	Arg	Thr	Val	Ile	His	His	Arg	Val	Pro	Asn	145	150	155	160
Glu	Glu	Asp	Pro	Ser	Leu	Asp	Arg	Pro	Phe	Ile	Ser	Glu	Gly	Thr	Thr	165	170	175	
Leu	Lys	Asp	Leu	Ile	Tyr	Asp	Met	Thr	Thr	Ser	Gly	Ser	Gly	Ser	Gly	180	185	190	
Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Arg	Thr	Ile	Val	Leu	Gln	195	200	205	
Glu	Ser	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly	Lys	Trp	210	215	220	

Arg	Gly	Glu	Glu	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu	Glu	Arg	225	230	235	240
Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu	Arg	His	245	250	255	
Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn	Gly	Thr	260	265	270	
Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly	Ser	Leu	275	280	285	
Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Val	Glu	Gly	Met	Ile	Lys	290	295	300	
Leu	Ala	Leu	Ser	Thr	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met	Glu	Ile	305	310	315	320
Val	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	325	330	335	
Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	Cys	Ile	Ala	Asp	Leu	340	345	350	
Gly	Leu	Ala	Val	Arg	His	Asp	Ser	Ala	Thr	Asp	Thr	Ile	Asp	Ile	Ala	355	360	365	
Pro	Asn	His	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	370	375	380	
Asp	Asp	Ser	Ile	Asn	Met	Lys	His	Phe	Glu	Ser	Phe	Lys	Arg	Ala	Asp	385	390	395	400
Ile	Tyr	Ala	Met	Gly	Leu	Val	Phe	Trp	Glu	Ile	Ala	Arg	Arg	Cys	Ser	405	410	415	
Ile	Gly	Gly	Ile	His	Glu	Asp	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asp	Leu	Val	420	425	430	
Pro	Ser	Asp	Pro	Ser	Val	Glu	Glu	Met	Arg	Lys	Val	Val	Cys	Glu	Gln	435	440	445	
Lys	Leu	Arg	Pro	Asn	Ile	Pro	Asn	Arg	Trp	Gln	Ser	Cys	Glu	Ala	Leu	450	455	460	
Arg	Val	Met	Ala	Lys	Ile	Met	Arg	Glu	Cys	Trp	Tyr	Ala	Asn	Gly	Ala	465	470	475	480
Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ser	Gln	Leu	Ser	485	490	495	
Gln	Gln	Glu	Gly	Ile	Lys	Met										500			

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 241..1746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GAGAGCACAG CCCTTCCCAG TCCCCGGAGC CGCCGCGCCA CGCGCGCATG ATCAAGACCT	60
TTTCCCCGGC CCCACAGGGC CTCTGGACGT GAGACCCCGG CCGCCTCCGC AAGGAGAGGC	120
GGGGGTCGAG TCGCCCTGTC CAAAGGCCTC AATCTAAACA ATCTTGATTCT CTGTTGCCGG	180
CTGGCGGGAC CCTGAATGGC AGGAAATCTC ACCACATCTC TTCTCCTATC TCCAAGGACC	240
ATG ACC TTG GGG AGC TTC AGA AGG GGC CTT TTG ATG CTG TCG GTG GCC	288
Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Leu Met Leu Ser Val Ala	
1 5 10 15	
TTG GGC CTA ACC CAG GGG AGA CTT GCG AAG CCT TCC AAG CTG GTG AAC	336
Leu Gly Leu Thr Gln Gly Arg Leu Ala Lys Pro Ser Lys Leu Val Asn	
20 25 30	
TGC ACT TGT GAG AGC CCA CAC TGC AAG AGA CCA TTC TGC CAG GGG TCA	384
Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser	
35 40 45	
TGG TGC ACA GTG GTG CTG GTT CGA GAG CAG GGC AGG CAC CCC CAG GTC	432
Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val	
50 55 60	
TAT CGG GGC TGT GGG AGC CTG AAC CAG GAG CTC TGC TTG GGA CGT CCC	480
Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro	
65 70 75 80	
ACG GAG TTT CTG AAC CAT CAC TGC TGC TAT AGA TCC TTC TGC AAC CAC	528
Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His	
85 90 95	
AAC GTG TCT CTG ATG CTG GAG GCC ACC CAA ACT CCT TCG GAG GAG CCA	576
Asn Val Ser Leu Met Leu Glu Ala Thr Gln Thr Pro Ser Glu Glu Pro	
100 105 110	
GAA GTT GAT GCC CAT CTG CCT CTG ATC CTG GGT CCT GTG CTG GCC TTG	624
Glu Val Asp Ala His Leu Pro Leu Ile Leu Gly Pro Val Leu Ala Leu	
115 120 125	
CCG GTC CTG GTG GCC CTG GGT GCT CTG GGC TTG TGG CGT GTC CGG CGG	672
Pro Val Leu Val Ala Leu Gly Ala Leu Gly Leu Trp Arg Val Arg Arg	
130 135 140	
AGG CAG GAG AAG CAG CGG GAT TTG CAC AGT GAC CTG GGC GAG TCC AGT	720
Arg Gln Glu Lys Gln Arg Asp Leu His Ser Asp Leu Gly Glu Ser Ser	

145	150	155	160	
CTC ATC CTG AAG GCA TCT GAA CAG GCA GAC AGC ATG TTG GGG GAC TTC				768
Leu Ile Leu Lys Ala Ser Glu Gln Ala Asp Ser Met Leu Gly Asp Phe	165	170	175	
CTG GAC AGC GAC TGT ACC ACG GGC AGC GGC TCG GGG CTC CCC TTC TTG				816
Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu	180	185	190	
GTG CAG AGG ACG GTA GCT CGG CAG GTT GCG CTG GTA GAG TGT GTG GGA				864
Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly	195	200	205	
AAG GGC CGA TAT GGC GAG GTG TGG CGC GGT TCG TGG CAT GGC GAA AGC				912
Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp His Gly Glu Ser	210	215	220	
GTG GCG GTC AAG ATT TTC TCC TCA CGA GAT GAG CAG TCC TGG TTC CGG				960
Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg	225	230	235	240
GAG ACG GAG ATC TAC AAC ACA GTT CTG CTT AGA CAC GAC AAC ATC CTA				1008
Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu	245	250	255	
GGC TTC ATC GCC TCC GAC ATG ACT TCG CGG AAC TCG AGC ACG CAG CTG				1056
Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu	260	265	270	
TGG CTC ATC ACC CAC TAC CAT GAA CAC GGC TCC CTC TAT GAC TTT CTG				1104
Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu	275	280	285	
CAG AGG CAG ACG CTG GAG CCC CAG TTG GCC CTG AGG CTA GCT GTG TCC				1152
Gln Arg Gln Thr Leu Glu Pro Gln Leu Ala Leu Arg Leu Ala Val Ser	290	295	300	
CCG GCC TGC GGC CTG GCG CAC CTA CAT GTG GAG ATC TTT GGC ACT CAA				1200
Pro Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln	305	310	315	320
GGC AAA CCA GCC ATT GCC CAT CGT GAC CTC AAG AGT CGC AAT GTG CTG				1248
Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Arg Asn Val Leu	325	330	335	
GTC AAG AGT AAC TTG CAG TGT TGC ATT GCA GAC CTG GGA CTG GCT GTG				1296
Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val	340	345	350	
ATG CAC TCA CAA AGC AAC GAG TAC CTG GAT ATC GGC AAC ACA CCC CGA				1344
Met His Ser Gln Ser Asn Glu Tyr Leu Asp Ile Gly Asn Thr Pro Arg	355	360	365	

GTG GGT ACC AAA AGA TAC ATG GCA CCC GAG GTG CTG GAT GAG CAC ATC	1392
Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu His Ile	
370 375 380	
CGC ACA GAC TGC TTT GAG TCG TAC AAG TGG ACA GAC ATC TGG GCC TTT	1440
Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe	
385 390 395 400	
GGC CTA GTG CTA TGG GAG ATC GCC CGG CGG ACC ATC ATC AAT GGC ATT	1488
Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile	
405 410 415	
GTG GAG GAT TAC AGG CCA CCT TTC TAT GAC ATG GTA CCC AAT GAC CCC	1536
Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro	
420 425 430	
AGT TTT GAG GAC ATG AAA AAG GTG GTG TGC GTT GAC CAG CAG ACA CCC	1584
Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro	
435 440 445	
ACC ATC CCT AAC CGG CTG GCT GCA GAT CCG GTC CTC TCC GGG CTG GCC	1632
Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala	
450 455 460	
CAG ATG ATG AGA GAG TGC TGG TAC CCC AAC CCC TCT GCT CGC CTC ACC	1680
Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr	
465 470 475 480	
GCA CTG CGC ATA AAG AAG ACA TTG CAG AAG CTC AGT CAC AAT CCA GAG	1728
Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu	
485 490 495	
AAG CCC AAA GTG ATT CAC TAGCCCAGGG CCACCAGGCT TCCTCTGCCT	1776
Lys Pro Lys Val Ile His	
500	
AAAGTGTGTG CTGGGGAAGA AGACATAGCC TGTCTGGGTA GAGGGAGTGA AGAGAGTGTG	1836
CACGCTGCCC TGTGTGTGCC TGCTCAGCTT GCTCCCAGCC CATCCAGCCA AAAATACAGC	1896
TGAGCTGAAA TTCAAAAAAA AAAAAA	1922

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Leu Met Leu Ser Val Ala

1				5				10					15			
Leu	Gly	Leu	Thr	Gln	Gly	Arg	Leu	Ala	Lys	Pro	Ser	Lys	Leu	Val	Asn	
			20					25					30			
Cys	Thr	Cys	Glu	Ser	Pro	His	Cys	Lys	Arg	Pro	Phe	Cys	Gln	Gly	Ser	
		35					40					45				
Trp	Cys	Thr	Val	Val	Leu	Val	Arg	Glu	Gln	Gly	Arg	His	Pro	Gln	Val	
	50					55					60					
Tyr	Arg	Gly	Cys	Gly	Ser	Leu	Asn	Gln	Glu	Leu	Cys	Leu	Gly	Arg	Pro	
65					70					75					80	
Thr	Glu	Phe	Leu	Asn	His	His	Cys	Cys	Tyr	Arg	Ser	Phe	Cys	Asn	His	
				85					90					95		
Asn	Val	Ser	Leu	Met	Leu	Glu	Ala	Thr	Gln	Thr	Pro	Ser	Glu	Glu	Pro	
			100				105						110			
Glu	Val	Asp	Ala	His	Leu	Pro	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	Leu	
	115					120					125					
Pro	Val	Leu	Val	Ala	Leu	Gly	Ala	Leu	Gly	Leu	Trp	Arg	Val	Arg	Arg	
	130					135					140					
Arg	Gln	Glu	Lys	Gln	Arg	Asp	Leu	His	Ser	Asp	Leu	Gly	Glu	Ser	Ser	
145				150					155						160	
Leu	Ile	Leu	Lys	Ala	Ser	Glu	Gln	Ala	Asp	Ser	Met	Leu	Gly	Asp	Phe	
				165					170					175		
Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu	
		180					185						190			
Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly	
	195						200					205				
Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Ser	Trp	His	Gly	Glu	Ser	
	210					215					220					
Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	Arg	
225				230					235						240	
Glu	Thr	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	Leu	
				245					250					255		
Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	Leu	
		260					265						270			
Trp	Leu	Ile	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	Leu	
	275						280					285				
Gln	Arg	Gln	Thr	Leu	Glu	Pro	Gln	Leu	Ala	Leu	Arg	Leu	Ala	Val	Ser	
	290					295					300					
Pro	Ala	Cys	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	Gln	
305				310					315						320	
Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Arg	Asn	Val	Leu	
				325					330					335		
Val	Lys	Ser	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	
		340					345						350			
Met	His	Ser	Gln	Ser	Asn	Glu	Tyr	Leu	Asp	Ile	Gly	Asn	Thr	Pro	Arg	
	355					360						365				
Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	His	Ile	
	370					375					380					
Arg	Thr	Asp	Cys	Phe	Glu	Ser	Tyr	Lys	Trp	Thr	Asp	Ile	Trp	Ala	Phe	
385				390					395						400	
Gly	Leu	Val	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Thr	Ile	Ile	Asn	Gly	Ile	
				405					410					415		
Val	Glu	Asp	Tyr	Arg	Pro	Pro	Phe	Tyr	Asp	Met	Val	Pro	Asn	Asp	Pro	
	420						425						430			
Ser	Phe	Glu	Asp	Met	Lys	Lys	Val	Val	Cys	Val	Asp	Gln	Gln	Thr	Pro	

40	45	50	
ACC TTG CCT TTC TTA AAG TGC TAT TGC TCA GGA CAC TGC CCA GAT GAT			426
Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser Gly His Cys Pro Asp Asp			
55	60	65	70
GCT ATT AAT AAC ACA TGC ATA ACT AAT GGC CAT TGC TTT GCC ATT ATA			474
Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly His Cys Phe Ala Ile Ile			
	75	80	85
GAA GAA GAT GAT CAG GGA GAA ACC ACA TTA ACT TCT GGG TGT ATG AAG			522
Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu Thr Ser Gly Cys Met Lys			
	90	95	100
TAT GAA GGC TCT GAT TTT CAA TGC AAG GAT TCA CCG AAA GCC CAG CTA			570
Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp Ser Pro Lys Ala Gln Leu			
	105	110	115
CGC AGG ACA ATA GAA TGT TGT CGG ACC AAT TTG TGC AAC CAG TAT TTG			618
Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn Leu Cys Asn Gln Tyr Leu			
	120	125	130
CAG CCT ACA CTG CCC CCT GTT GTT ATA GGT CCG TTC TTT GAT GGC AGC			666
Gln Pro Thr Leu Pro Pro Val Val Ile Gly Pro Phe Phe Asp Gly Ser			
	135	140	145
ATC CGA TGG CTG GTT GTG CTC ATT TCC ATG GCT GTC TGT ATA GTT GCT			714
Ile Arg Trp Leu Val Val Leu Ile Ser Met Ala Val Cys Ile Val Ala			
	155	160	165
ATG ATC ATC TTC TCC AGC TGC TTT TGC TAT AAG CAT TAT TGT AAG AGT			762
Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr Lys His Tyr Cys Lys Ser			
	170	175	180
ATC TCA AGC AGG GGT CGT TAC AAC CGT GAT TTG GAA CAG GAT GAA GCA			810
Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp Leu Glu Gln Asp Glu Ala			
	185	190	195
TTT ATT CCA GTA GGA GAA TCA TTG AAA GAC CTG ATT GAC CAG TCC CAA			858
Phe Ile Pro Val Gly Glu Ser Leu Lys Asp Leu Ile Asp Gln Ser Gln			
	200	205	210
AGC TCT GGG AGT GGA TCT GGA TTG CCT TTA TTG GTT CAG CGA ACT ATT			906
Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile			
	215	220	225
GCC AAA CAG ATT CAG ATG GTT CGG CAG GTT GGT AAA GGC CGC TAT GGA			954
Ala Lys Gln Ile Gln Met Val Arg Gln Val Gly Lys Gly Arg Tyr Gly			
	235	240	245
GAA GTA TGG ATG GGT AAA TGG CGT GGT GAA AAA GTG GCT GTC AAA GTG			1002
Glu Val Trp Met Gly Lys Trp Arg Gly Glu Lys Val Ala Val Lys Val			
	250	255	260

TTT TTT ACC ACT GAA GAA GCT AGC TGG TTT AGA GAA ACA GAA ATC TAC	1050
Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr	
265 270 275	
CAG ACG GTG TTA ATG CGT CAT GAA AAT ATA CTT GGT TTT ATA GCT GCA	1098
Gln Thr Val Leu Met Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala	
280 285 290	
GAC ATT AAA GGC ACT GGT TCC TGG ACT CAG CTG TAT TTG ATT ACT GAT	1146
Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp	
295 300 305 310	
TAC CAT GAA AAT GGA TCT CTC TAT GAC TTC CTG AAA TGT GCC ACA CTA	1194
Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe Leu Lys Cys Ala Thr Leu	
315 320 325	
GAC ACC AGA GCC CTA CTC AAG TTA GCT TAT TCT GCT GCT TGT GGT CTG	1242
Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr Ser Ala Ala Cys Gly Leu	
330 335 340	
TGC CAC CTC CAC ACA GAA ATT TAT GGT ACC CAA GGG AAG CCT GCA ATT	1290
Cys His Leu His Thr Glu Ile Tyr Gly Thr Gln Gly Lys Pro Ala Ile	
345 350 355	
GCT CAT CGA GAC CTG AAG AGC AAA AAC ATC CTT ATT AAG AAA AAT GGA	1338
Ala His Arg Asp Leu Lys Ser Lys Asn Ile Leu Ile Lys Lys Asn Gly	
360 365 370	
AGT TGC TGT ATT GCT GAC CTG GGC CTA GCT GTT AAA TTC AAC AGT GAT	1386
Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Lys Phe Asn Ser Asp	
375 380 385 390	
ACA AAT GAA GTT GAC ATA CCC TTG AAT ACC AGG GTG GGC ACC AAG CGG	1434
Thr Asn Glu Val Asp Ile Pro Leu Asn Thr Arg Val Gly Thr Lys Arg	
395 400 405	
TAC ATG GCT CCA GAA GTG CTG GAT GAA AGC CTG AAT AAA AAC CAT TTC	1482
Tyr Met Ala Pro Glu Val Leu Asp Glu Ser Leu Asn Lys Asn His Phe	
410 415 420	
CAG CCC TAC ATC ATG GCT GAC ATC TAT AGC TTT GGT TTG ATC ATT TGG	1530
Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser Phe Gly Leu Ile Ile Trp	
425 430 435	
GAA ATG GCT CGT CGT TGT ATT ACA GGA GGA ATC GTG GAG GAA TAT CAA	1578
Glu Met Ala Arg Arg Cys Ile Thr Gly Gly Ile Val Glu Glu Tyr Gln	
440 445 450	
TTA CCA TAT TAC AAC ATG GTG CCC AGT GAC CCA TCC TAT GAG GAC ATG	1626
Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp Pro Ser Tyr Glu Asp Met	
455 460 465 470	
CGT GAG GTT GTG TGT GTG AAA CGC TTG CGG CCA ATC GTG TCT AAC CGC	1674

Arg	Glu	Val	Val	Cys	Val	Lys	Arg	Leu	Arg	Pro	Ile	Val	Ser	Asn	Arg	
				475					480					485		
TGG	AAC	AGC	GAT	GAA	TGT	CTT	CGA	GCA	GTT	TTG	AAG	CTA	ATG	TCA	GAA	1722
Trp	Asn	Ser	Asp	Glu	Cys	Leu	Arg	Ala	Val	Leu	Lys	Leu	Met	Ser	Glu	
			490					495					500			
TGT	TGG	GCC	CAT	AAT	CCA	GCC	TCC	AGA	CTC	ACA	GCT	TTG	AGA	ATC	AAG	1770
Cys	Trp	Ala	His	Asn	Pro	Ala	Ser	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	
		505						510				515				
AAG	ACA	CTT	GCA	AAA	ATG	GTT	GAA	TCC	CAG	GAT	GTA	AAG	ATT			1812
Lys	Thr	Leu	Ala	Lys	Met	Val	Glu	Ser	Gln	Asp	Val	Lys	Ile			
		520						525				530				
TGACAATTAA	ACAATTTTGA	GGGAGAATTT	AGACTGCAAG	AACTTCTTCA	CCCAAGGAAT											1872
GGGTGGGATT	AGCATGGAAT	AGGATGTTGA	CTTGGTTTCC	AGACTCCTTC	CTCTACATCT											1932
TCACAGGCTG	CTAACAGTAA	ACCTTACCGT	ACTCTACAGA	ATACAAGATT	GGAAC TTGGA											1992
ACTTCAAACA	TGTCATTCTT	TATATATGAC	AGCTTTGTTT	TAATGTGGGG	TTTTTTTGT											2052
TGCTTTTTTTT	GTTTTGTT															2070

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met	Thr	Gln	Leu	Tyr	Thr	Tyr	Ile	Arg	Leu	Leu	Gly	Ala	Cys	Leu	Phe	
1				5					10					15		
Ile	Ile	Ser	His	Val	Gln	Gly	Gln	Asn	Leu	Asp	Ser	Met	Leu	His	Gly	
			20					25					30			
Thr	Gly	Met	Lys	Ser	Asp	Leu	Asp	Gln	Lys	Lys	Pro	Glu	Asn	Gly	Val	
		35					40					45				
Thr	Leu	Ala	Pro	Glu	Asp	Thr	Leu	Pro	Phe	Leu	Lys	Cys	Tyr	Cys	Ser	
	50					55					60					
Gly	His	Cys	Pro	Asp	Asp	Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly	
65					70				75					80		
His	Cys	Phe	Ala	Ile	Ile	Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu	
			85					90						95		
Thr	Ser	Gly	Cys	Met	Lys	Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp	
		100					105					110				
Ser	Pro	Lys	Ala	Gln	Leu	Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn	
		115					120					125				
Leu	Cys	Asn	Gln	Tyr	Leu	Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly	
	130					135					140					

Pro	Phe	Phe	Asp	Gly	Ser	Ile	Arg	Trp	Leu	Val	Val	Leu	Ile	Ser	Met
145					150					155					160
Ala	Val	Cys	Ile	Val	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr
				165					170						175
Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Gly	Arg	Tyr	Asn	Arg	Asp
			180				185						190		
Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp
		195					200					205			
Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu
	210					215					220				
Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val
225					230					235					240
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu
			245						250					255	
Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe
			260					265					270		
Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile
		275					280					285			
Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln
	290					295					300				
Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe
305					310					315					320
Leu	Lys	Cys	Ala	Thr	Leu	Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	Ala	Tyr
			325						330					335	
Ser	Ala	Ala	Cys	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Tyr	Gly	Thr
			340					345					350		
Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile
	355						360					365			
Leu	Ile	Lys	Lys	Asn	Gly	Ser	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala
	370					375					380				
Val	Lys	Phe	Asn	Ser	Asp	Thr	Asn	Glu	Val	Asp	Ile	Pro	Leu	Asn	Thr
385					390					395					400
Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Ser
			405						410					415	
Leu	Asn	Lys	Asn	His	Phe	Gln	Pro	Tyr	Ile	Met	Ala	Asp	Ile	Tyr	Ser
		420						425					430		
Phe	Gly	Leu	Ile	Ile	Trp	Glu	Met	Ala	Arg	Arg	Cys	Ile	Thr	Gly	Gly
	435						440					445			
Ile	Val	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asn	Met	Val	Pro	Ser	Asp
	450					455					460				
Pro	Ser	Tyr	Glu	Asp	Met	Arg	Glu	Val	Val	Cys	Val	Lys	Arg	Leu	Arg
465					470					475					480
Pro	Ile	Val	Ser	Asn	Arg	Trp	Asn	Ser	Asp	Glu	Cys	Leu	Arg	Ala	Val
			485						490					495	
Leu	Lys	Leu	Met	Ser	Glu	Cys	Trp	Ala	His	Asn	Pro	Ala	Ser	Arg	Leu
		500						505					510		
Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ala	Lys	Met	Val	Glu	Ser	Gln
	515						520					525			
Asp	Val	Lys	Ile												
	530														

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 10..1524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CGCGGTTAC ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT	48
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu	
1 5 10	
GTT GTC CTC CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG ATC	96
Val Val Leu Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Ile	
15 20 25	
CAG GCT CTG CTG TGT GCG TGC ACC AGC TGC CTA CAG ACC AAC TAC ACC	144
Gln Ala Leu Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr	
30 35 40 45	
TGT GAG ACA GAT GGG GCT TGC ATG GTC TCC ATC TTT AAC CTG GAT GGC	192
Cys Glu Thr Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly	
50 55 60	
GTG GAG CAC CAT GTA CGT ACC TGC ATC CCC AAG GTG GAG CTG GTT CCT	240
Val Glu His His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro	
65 70 75	
GCT GGA AAG CCC TTC TAC TGC CTG AGT TCA GAG GAT CTG CGC AAC ACA	288
Ala Gly Lys Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr	
80 85 90	
CAC TGC TGC TAT ATT GAC TTC TGC AAC AAG ATT GAC CTC AGG GTC CCC	336
His Cys Cys Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro	
95 100 105	
AGC GGA CAC CTC AAG GAG CCT GCG CAC CCC TCC ATG TGG GGC CCT GTG	384
Ser Gly His Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val	
110 115 120 125	

GAG CTG GTC GGC ATC ATC GCC GGC CCC GTC TTC CTC CTC TTC CTT ATC Glu Leu Val Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile 130 135 140	432
ATT ATC ATC GTC TTC CTG GTC ATC AAC TAT CAC CAG CGT GTC TAC CAT Ile Ile Ile Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His 145 150 155	480
AAC CGC CAG AGG TTG GAC ATG GAG GAC CCC TCT TGC GAG ATG TGT CTC Asn Arg Gln Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu 160 165 170	528
TCC AAA GAC AAG ACG CTC CAG GAT CTC GTC TAC GAC CTC TCC ACG TCA Ser Lys Asp Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser 175 180 185	576
GGG TCT GGC TCA GGG TTA CCC CTT TTT GTC CAG CGC ACA GTG GCC CGA Gly Ser Gly Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg 190 195 200 205	624
ACC ATT GTT TTA CAA GAG ATT ATC GGC AAG GGC CGG TTC GGG GAA GTA Thr Ile Val Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val 210 215 220	672
TGG CGT GGT CGC TGG AGG GGT GGT GAC GTG GCT GTG AAA ATC TTC TCT Trp Arg Gly Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser 225 230 235	720
TCT CGT GAA GAA CGG TCT TGG TTC CGT GAA GCA GAG ATC TAC CAG ACC Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr 240 245 250	768
GTC ATG CTG CGC CAT GAA AAC ATC CTT GGC TTT ATT GCT GCT GAC AAT Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn 255 260 265	816
AAA GAT AAT GGC ACC TGG ACC CAG CTG TGG CTT GTC TCT GAC TAT CAC Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His 270 275 280 285	864
GAG CAT GGC TCA CTG TTT GAT TAT CTG AAC CGC TAC ACA GTG ACC ATT Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile 290 295 300	912
GAG GGA ATG ATT AAG CTA GCC TTG TCT GCA GCC AGT GGT TTG GCA CAC Glu Gly Met Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His 305 310 315	960
CTG CAT ATG GAG ATT GTG GGC ACT CAA GGG AAG CCG GGA ATT GCT CAT Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His 320 325 330	1008
CGA GAC TTG AAG TCA AAG AAC ATC CTG GTG AAA AAA AAT GGC ATG TGT Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys	1056

335	340	345	
GCC ATT GCA GAC CTG GGC CTG GCT GTC CGT CAT GAT GCG GTC ACT GAC			1104
Ala Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp			
350	355	360	365
ACC ATA GAC ATT GCT CCA AAT CAG AGG GTG GGG ACC AAA CGA TAC ATG			1152
Thr Ile Asp Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met			
	370	375	380
GCT CCT GAA GTC CTT GAC GAG ACA ATC AAC ATG AAG CAC TTT GAC TCC			1200
Ala Pro Glu Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser			
	385	390	395
TTC AAA TGT GCC GAC ATC TAT GCC CTC GGG CTT GTC TAC TGG GAG ATT			1248
Phe Lys Cys Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile			
	400	405	410
GCA CGA AGA TGC AAT TCT GGA GGA GTC CAT GAA GAC TAT CAA CTG CCG			1296
Ala Arg Arg Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro			
	415	420	425
TAT TAC GAC TTA GTG CCC TCC GAC CCT TCC ATT GAG GAG ATG CGA AAG			1344
Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys			
	430	435	440
GTT GTA TGT GAC CAG AAG CTA CGG CCC AAT GTC CCC AAC TGG TGG CAG			1392
Val Val Cys Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln			
	450	455	460
AGT TAT GAG GCC TTG CGA GTG ATG GGA AAG ATG ATG CGG GAG TGC TGG			1440
Ser Tyr Glu Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp			
	465	470	475
TAC GCC AAT GGT GCT GCC CGT CTG ACA GCT CTG CGC ATC AAG AAG ACT			1488
Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr			
	480	485	490
CTG TCC CAG CTA AGC GTG CAG GAA GAT GTG AAG ATT TAAGCTGTTC			1534
Leu Ser Gln Leu Ser Val Gln Glu Asp Val Lys Ile			
	495	500	505
CTCTGCCTAC ACAAAGAACC TGGGCAGTGA GGATGACTGC AGCCACCGTG CAAGCGTCGT			1594
GGAGGCCTAT CCTCTTGTTT CTGCCCCGCC CTCTGGCAGA GCCCTGGCCT GCAAGAGGGA			1654
CAGAGCCTGG GAGACGCGCG CACTCCCGTT GGGTTTGAGA CAGACACTTT TTATATTTAC			1714
CTCCTGATGG CATGGAGACC TGAGCAAATC ATGTAGTCAC TCAATGCCAC AACTCAAAC			1774
GCTTCAGTGG GAAGTACAGA GACCCAGTGC ATTGCGTGTG CAGGAGCGTG AGGTGCTGGG			1834
CTCGCCAGGA GCGGCCCCCA TACCTTGTGG TCCACTGGGC TGCAGGTTTT CCTCCAGGGA			1894

CCAGTCAACT GGCATCAAGA TATTGAGAGG AACCGGAAGT TTCTCCCTCC TTCCCGTAGC 1954
AGTCCTGAGC CACACCATCC TTCTCATGGA CATCCGGAGG ACTGCCCCCTA GAGACACAAC 2014
CTGCTGCCTG TCTGTCCAGC CAAGTGCGCA TGTGCCGAGG TGTGTCCCAC ATTGTGCCTG 2074
GTCTGTGCCA CGCCCGTGTG TGTGTGTGTG TGTGTGAGTG AGTGTGTGTG TGTACACTTA 2134
ACCTGCTTGA GCTTCTGTGC ATGTGT 2160

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met	Ala	Glu	Ser	Ala	Gly	Ala	Ser	Ser	Phe	Phe	Pro	Leu	Val	Val	Leu	
1				5					10					15		
Leu	Leu	Ala	Gly	Ser	Gly	Gly	Ser	Gly	Pro	Arg	Gly	Ile	Gln	Ala	Leu	
			20					25					30			
Leu	Cys	Ala	Cys	Thr	Ser	Cys	Leu	Gln	Thr	Asn	Tyr	Thr	Cys	Glu	Thr	
			35				40					45				
Asp	Gly	Ala	Cys	Met	Val	Ser	Ile	Phe	Asn	Leu	Asp	Gly	Val	Glu	His	
			50			55				60						
His	Val	Arg	Thr	Cys	Ile	Pro	Lys	Val	Glu	Leu	Val	Pro	Ala	Gly	Lys	
					70				75					80		
Pro	Phe	Tyr	Cys	Leu	Ser	Ser	Glu	Asp	Leu	Arg	Asn	Thr	His	Cys	Cys	
				85				90						95		
Tyr	Ile	Asp	Phe	Cys	Asn	Lys	Ile	Asp	Leu	Arg	Val	Pro	Ser	Gly	His	
			100				105					110				
Leu	Lys	Glu	Pro	Ala	His	Pro	Ser	Met	Trp	Gly	Pro	Val	Glu	Leu	Val	
			115				120					125				
Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	Ile	Ile	Ile	
			130			135					140					
Val	Phe	Leu	Val	Ile	Asn	Tyr	His	Gln	Arg	Val	Tyr	His	Asn	Arg	Gln	
					150				155					160		
Arg	Leu	Asp	Met	Glu	Asp	Pro	Ser	Cys	Glu	Met	Cys	Leu	Ser	Lys	Asp	
				165				170						175		
Lys	Thr	Leu	Gln	Asp	Leu	Val	Tyr	Asp	Leu	Ser	Thr	Ser	Gly	Ser	Gly	
			180				185					190				
Ser	Gly	Leu	Pro	Leu	Phe	Val	Gln	Arg	Thr	Val	Ala	Arg	Thr	Ile	Val	
		195					200					205				
Leu	Gln	Glu	Ile	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly	
		210				215					220					
Arg	Trp	Arg	Gly	Gly	Asp	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu	
					230				235					240		
Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu	
				245				250						255		

(B) LOCATION: 187..1692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AAGCGGCGGC AGAAGTTGCC GGC GTGGTGC TCGTAGTGAG GGCGCGGAGG ACCCGGGACC	60
TGGGAAGCGG CGGCGGGTTA ACTTCGGCTG AATCACAACC ATTTGGCGCT GAGCTATGAC	120
AAGAGAGCAA ACAAAAAGTT AAAGGAGCAA CCCGGCCATA AGTGAAGAGA GAAGTTTATT	180
GATAAC ATG CTC TTA CGA AGC TCT GGA AAA TTA AAT GTG GGC ACC AAG	228
Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys	
1 5 10	
AAG GAG GAT GGA GAG AGT ACA GCC CCC ACC CCT CGG CCC AAG ATC CTA	276
Lys Glu Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu	
15 20 25 30	
CGT TGT AAA TGC CAC CAC CAC TGT CCG GAA GAC TCA GTC AAC AAT ATC	324
Arg Cys Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile	
35 40 45	
TGC AGC ACA GAT GGG TAC TGC TTC ACG ATG ATA GAA GAA GAT GAC TCT	372
Cys Ser Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser	
50 55 60	
GGA ATG CCT GTT GTC ACC TCT GGA TGT CTA GGA CTA GAA GGG TCA GAT	420
Gly Met Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp	
65 70 75	
TTT CAA TGT CGT GAC ACT CCC ATT CCT CAT CAA AGA AGA TCA ATT GAA	468
Phe Gln Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu	
80 85 90	
TGC TGC ACA GAA AGG AAT GAG TGT AAT AAA GAC CTC CAC CCC ACT CTG	516
Cys Cys Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu	
95 100 105 110	
CCT CCT CTC AAG GAC AGA GAT TTT GTT GAT GGG CCC ATA CAC CAC AAG	564
Pro Pro Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys	
115 120 125	
GCC TTG CTT ATC TCT GTG ACT GTC TGT AGT TTA CTC TTG GTC CTC ATT	612
Ala Leu Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile	
130 135 140	
ATT TTA TTC TGT TAC TTC AGG TAT AAA AGA CAA GAA GCC CGA CCT CGG	660
Ile Leu Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg	
145 150 155	
TAC AGC ATT GGG CTG GAG CAG GAC GAG ACA TAC ATT CCT CCT GGA GAG	708
Tyr Ser Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu	
160 165 170	

TCC CTG AGA GAC TTG ATC GAG CAG TCT CAG AGC TCG GGA AGT GGA TCA	756
Ser Leu Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser	
175 180 185 190	
GGC CTC CCT CTG CTG GTC CAA AGG ACA ATA GCT AAG CAA ATT CAG ATG	804
Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met	
195 200 205	
GTG AAG CAG ATT GGA AAA GGC CGC TAT GGC GAG GTG TGG ATG GGA AAG	852
Val Lys Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys	
210 215 220	
TGG CGT GGA GAA AAG GTG GCT GTG AAA GTG TTC TTC ACC ACG GAG GAA	900
Trp Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu	
225 230 235	
GCC AGC TGG TTC CGA GAG ACT GAG ATA TAT CAG ACG GTC CTG ATG CGG	948
Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg	
240 245 250	
CAT GAG AAT ATT CTG GGG TTC ATT GCT GCA GAT ATC AAA GGG ACT GGG	996
His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly	
255 260 265 270	
TCC TGG ACT CAG TTG TAC CTC ATC ACA GAC TAT CAT GAA AAC GGC TCC	1044
Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser	
275 280 285	
CTT TAT GAC TAT CTG AAA TCC ACC ACC TTA GAC GCA AAG TCC ATG CTG	1092
Leu Tyr Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu	
290 295 300	
AAG CTA GCC TAC TCC TCT GTC AGC GGC CTA TGC CAT TTA CAC ACG GAA	1140
Lys Leu Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu	
305 310 315	
ATC TTT AGC ACT CAA GGC AAG CCA GCA ATC GCC CAT CGA GAC TTG AAA	1188
Ile Phe Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys	
320 325 330	
AGT AAA AAC ATC CTG GTG AAG AAA AAT GGA ACT TGC TGC ATA GCA GAC	1236
Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp	
335 340 345 350	
CTG GGC TTG GCT GTC AAG TTC ATT AGT GAC ACA AAT GAG GTT GAC ATC	1284
Leu Gly Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile	
355 360 365	
CCA CCC AAC ACC CGG GTT GGC ACC AAG CGC TAT ATG CCT CCA GAA GTG	1332
Pro Pro Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val	
370 375 380	
CTG GAC GAG AGC TTG AAT AGA AAC CAT TTC CAG TCC TAC ATT ATG GCT	1380
Leu Asp Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala	

385	390	395	
GAC ATG TAC AGC TTT GGA CTC ATC CTC TGG GAG ATT GCA AGG AGA TGT			1428
Asp Met Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys			
400	405	410	
GTT TCT GGA GGT ATA GTG GAA GAA TAC CAG CTT CCC TAT CAC GAC CTG			1476
Val Ser Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu			
415	420	425	430
GTG CCC AGT GAC CCT TCT TAT GAG GAC ATG AGA GAA ATT GTG TGC ATG			1524
Val Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met			
	435	440	445
AAG AAG TTA CGG CCT TCA TTC CCC AAT CGA TGG AGC AGT GAT GAG TGT			1572
Lys Lys Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys			
	450	455	460
CTC AGG CAG ATG GGG AAG CTT ATG ACA GAG TGC TGG GCG CAG AAT CCT			1620
Leu Arg Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro			
	465	470	475
GCC TCC AGG CTG ACG GCC CTG AGA GTT AAG AAA ACC CTT GCC AAA ATG			1668
Ala Ser Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met			
	480	485	490
TCA GAG TCC CAG GAC ATT AAA CTC TGACGTCAGA TACTTGTGGA CAGAGCAAGA			1722
Ser Glu Ser Gln Asp Ile Lys Leu			
495	500		
ATTTACACAGA AGCATCGTTA GCCCAAGCCT TGAACGTTAG CCTACTGCCC AGTGAGTTCA			1782
GACTTTCCTG GAAGAGAGCA CGGTGGGCAG ACACAGAGGA ACCCAGAAAC ACGGATTCAT			1842
CATGGCTTTC TGAGGAGGAG AAACTGTTTG GGTAACCTGT TCAAGATATG ATGCATGTTG			1902
CTTTCTAAGA AAGCCCTGTA TTTTGAATTA CCATTTTTTTT ATAAAAAAAAA			1952

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met	Leu	Leu	Arg	Ser	Ser	Gly	Lys	Leu	Asn	Val	Gly	Thr	Lys	Lys	Glu
1				5					10					15	
Asp	Gly	Glu	Ser	Thr	Ala	Pro	Thr	Pro	Arg	Pro	Lys	Ile	Leu	Arg	Cys
			20					25					30		
Lys	Cys	His	His	His	Cys	Pro	Glu	Asp	Ser	Val	Asn	Asn	Ile	Cys	Ser

		35					40					45					
Thr	Asp	Gly	Tyr	Cys	Phe	Thr	Met	Ile	Glu	Glu	Asp	Asp	Ser	Gly	Met		
	50						55				60						
Pro	Val	Val	Thr	Ser	Gly	Cys	Leu	Gly	Leu	Glu	Gly	Ser	Asp	Phe	Gln		
65					70					75					80		
Cys	Arg	Asp	Thr	Pro	Ile	Pro	His	Gln	Arg	Arg	Ser	Ile	Glu	Cys	Cys		
				85					90					95			
Thr	Glu	Arg	Asn	Glu	Cys	Asn	Lys	Asp	Leu	His	Pro	Thr	Leu	Pro	Pro		
			100					105					110				
Leu	Lys	Asp	Arg	Asp	Phe	Val	Asp	Gly	Pro	Ile	His	His	Lys	Ala	Leu		
		115					120					125					
Leu	Ile	Ser	Val	Thr	Val	Cys	Ser	Leu	Leu	Leu	Val	Leu	Ile	Ile	Leu		
	130					135					140						
Phe	Cys	Tyr	Phe	Arg	Tyr	Lys	Arg	Gln	Glu	Ala	Arg	Pro	Arg	Tyr	Ser		
145					150					155					160		
Ile	Gly	Leu	Glu	Gln	Asp	Glu	Thr	Tyr	Ile	Pro	Pro	Gly	Glu	Ser	Leu		
				165					170					175			
Arg	Asp	Leu	Ile	Glu	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu		
			180					185					190				
Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Lys		
		195					200					205					
Gln	Ile	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg		
	210					215					220						
Gly	Glu	Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser		
225					230					235					240		
Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu		
				245					250					255			
Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp		
			260					265					270				
Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr		
		275					280					285					
Asp	Tyr	Leu	Lys	Ser	Thr	Thr	Leu	Asp	Ala	Lys	Ser	Met	Leu	Lys	Leu		
	290					295					300						
Ala	Tyr	Ser	Ser	Val	Ser	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Phe		
305					310					315					320		
Ser	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys		
				325					330					335			
Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	Cys	Ile	Ala	Asp	Leu	Gly		
			340					345					350				
Leu	Ala	Val	Lys	Phe	Ile	Ser	Asp	Thr	Asn	Glu	Val	Asp	Ile	Pro	Pro		
		355					360					365					
Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Pro	Pro	Glu	Val	Leu	Asp		
	370					375						380					
Glu	Ser	Leu	Asn	Arg	Asn	His	Phe	Gln	Ser	Tyr	Ile	Met	Ala	Asp	Met		
385					390					395							

465 470 475 480
Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met Ser Glu
 485 490 495
Ser Gln Asp Ile Lys Leu
 500

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GCGGATCCTG TTGTGAAGGN AATATGTG

28

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GCGATCCGTC GCAGTCAAAA TTTT

24

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCGGATCCGC GATATATTAA AAGCAA

26

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CGGAATTCTG GTGCCATATA

20

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATTCAAGGGC ACATCAACTT CATTTGTGTC ACTGTTG

37

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GCGGATCCAC CATGGCGGAG TCGGCC

26

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AACACCGGGC CGGCGATGAT

20

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gly Xaa Gly Xaa Xaa Gly

1

5

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Asp Phe Lys Ser Arg Asn

1

5

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Asp Leu Lys Ser Lys Asn
1 5

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Gly Thr Lys Arg Tyr Met
1 5

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Leu Asp Thr Leu Val Gly Lys Gly Arg Phe Ala Glu Val Tyr Lys Ala
5 10 15
Lys Leu Lys Gln Asn Thr Ser Glu Gln Phe Glu Thr Val Ala Val Lys
20 25 30
Ile Phe Pro Tyr Asp His Tyr Ala Ser Trp Lys Asp Arg Lys Asp Ile
35 40 45
Phe Ser Asp Ile Asn Leu Lys His Glu Asn Ile Leu Gln Phe Leu Thr
50 55 60
Ala Glu Glu Arg Lys Thr Glu Leu Gly Lys Gln Tyr Trp Leu Ile Thr
65 70 75 80
Ala Phe His Ala Lys Gly Asn Leu Gln Glu Tyr Leu Thr Arg His Val
85 90 95
Ile Ser Trp Glu Asp Leu Arg Asn Val Gly Ser Ser Leu Ala Arg Gly

			100					105				110					
Leu	Ser	His	Leu	His	Ser	Asp	His	Thr	Pro	Cys	Gly	Arg	Pro	Lys	Met		
		115						120				125					
Pro	Ile	Val	His	Arg	Asp	Leu	Lys	Ser	Ser	Asn	Ile	Leu	Val	Lys	Asn		
		130						135				140					
Asp	Leu	Thr	Cys	Cys	Leu	Cys	Asp	Phe	Gly	Leu	Ser	Leu	Arg	Leu	Gly		
145						150				155					160		
Pro	Tyr	Ser	Ser	Val	Asp	Asp	Leu	Ala	Asn	Ser	Gly	Gln	Val	Gly	Thr		
				165					170					175			
Ala	Arg	Tyr	Met	Ala	Pro												
			180														

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Leu	Leu	Glu	Ile	Lys	Ala	Arg	Gly	Arg	Phe	Gly	Cys	Val	Trp	Lys	Ala		
			5						10					15			
Gln	Leu	Met	Asn	Asp	Phe	Val	Ala	Val	Lys	Ile	Phe	Pro	Leu	Gln	Asp		
		20						25					30				
Lys	Gln	Ser	Trp	Gln	Ser	Glu	Arg	Glu	Ile	Phe	Ser	Thr	Pro	Gly	Met		
		35					40					45					
Lys	His	Glu	Asn	Leu	Leu	Gln	Phe	Ile	Ala	Ala	Glu	Lys	Arg	Gly	Ser		
		50				55					60						
Asn	Leu	Glu	Val	Glu	Leu	Trp	Leu	Ile	Thr	Ala	Phe	His	Asp	Lys	Gly		
65					70				75					80			
Ser	Leu	Thr	Asp	Tyr	Leu	Lys	Gly	Asn	Ile	Ile	Thr	Trp	Asn	Glu	Leu		
			85					90					95				
Cys	His	Val	Ala	Glu	Thr	Met	Ser	Arg	Gly	Leu	Ser	Tyr	Leu	His	Glu		
		100						105					110				
Asp	Val	Pro	Trp	Cys	Arg	Gly	Glu	Gly	His	Lys	Pro	Ser	Ile	Ala	His		
		115					120					125					
Arg	Asp	Phe	Lys	Ser	Lys	Asn	Val	Leu	Leu	Lys	Ser	Asp	Leu	Thr	Ala		
		130				135					140						
Val	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Val	Arg	Phe	Glu	Pro	Gly	Lys	Pro		
145					150				155					160			
Pro	Gly	Asp	Thr	His	Gly	Gln	Val	Gly	Thr	Arg	Arg	Tyr	Met	Ala	Pro		
				165				170					175				

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Leu	Leu	Glu	Val	Lys	Ala	Arg	Gly	Arg	Phe	Gly	Cys	Val	Trp	Lys	Ala	
				5					10					15		
Gln	Leu	Leu	Asn	Glu	Tyr	Val	Ala	Val	Lys	Ile	Phe	Pro	Ile	Gln	Asp	
			20					25					30			
Lys	Gln	Ser	Trp	Gln	Asn	Glu	Tyr	Glu	Val	Tyr	Ser	Leu	Pro	Gly	Met	
		35					40					45				
Lys	His	Glu	Asn	Ile	Leu	Gln	Phe	Ile	Gly	Ala	Glu	Lys	Arg	Gly	Thr	
	50					55					60					
Ser	Val	Asp	Val	Asp	Leu	Trp	Leu	Ile	Thr	Ala	Phe	His	Glu	Lys	Gly	
65					70					75					80	
Ser	Leu	Ser	Asp	Phe	Leu	Lys	Ala	Asn	Val	Val	Ser	Trp	Asn	Glu	Leu	
			85					90					95			
Cys	His	Ile	Ala	Glu	Thr	Met	Ala	Arg	Gly	Leu	Ala	Tyr	Leu	His	Glu	
		100						105					110			
Asp	Ile	Pro	Gly	Leu	Lys	Asp	Gly	His	Lys	Pro	Ala	Ile	Ser	His	Arg	
	115						120					125				
Asp	Ile	Lys	Ser	Lys	Asn	Val	Leu	Leu	Lys	Asn	Asn	Leu	Thr	Ala	Cys	
	130				135					140						
Ile	Ala	Asp	Phe	Gly	Leu	Ala	Leu	Lys	Phe	Glu	Ala	Gly	Lys	Ser	Ala	
145					150					155					160	
Gly	Asp	Thr	His	Gly	Gln	Val	Gly	Thr	Arg	Arg	Tyr	Met	Ala	Pro		
				165					170					175		

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: C. elegans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Leu	Thr	Gly	Arg	Val	Gly	Ser	Gly	Arg	Phe	Gly	Asn	Val	Ser	Arg	Gly	
				5					10					15		
Asp	Tyr	Arg	Gly	Glu	Ala	Val	Ala	Val	Lys	Val	Phe	Asn	Ala	Leu	Asp	
		20						25					30			
Glu	Pro	Ala	Phe	His	Lys	Glu	Thr	Glu	Ile	Phe	Glu	Thr	Arg	Met	Leu	
	35					40						45				
Arg	His	Pro	Asn	Val	Leu	Arg	Tyr	Ile	Gly	Ser	Asp	Arg	Val	Asp	Thr	

50		55		60																																																																															
Gly	Phe	Val	Thr	Glu	Leu	65		70		75		Ser	Leu	His	Asp	Phe	Leu			85		90		Tyr	Asn	Leu	Met	Arg	Ser			100		105		Gln	Ile	Gly	Gly	Ser	Lys			115		120		Asp	Ile	Lys	Ser	Lys	Asn			130		135		Ile	Gly	Asp	Leu	Gly	Leu	145				150		Asp	Ile	Ile	Ala	Asn	Glu					165	
65		70		75																																																																															
Ser	Leu	His	Asp	Phe	Leu			85		90		Tyr	Asn	Leu	Met	Arg	Ser			100		105		Gln	Ile	Gly	Gly	Ser	Lys			115		120		Asp	Ile	Lys	Ser	Lys	Asn			130		135		Ile	Gly	Asp	Leu	Gly	Leu	145				150		Asp	Ile	Ile	Ala	Asn	Glu					165													
		85		90																																																																															
Tyr	Asn	Leu	Met	Arg	Ser			100		105		Gln	Ile	Gly	Gly	Ser	Lys			115		120		Asp	Ile	Lys	Ser	Lys	Asn			130		135		Ile	Gly	Asp	Leu	Gly	Leu	145				150		Asp	Ile	Ile	Ala	Asn	Glu					165																									
		100		105																																																																															
Gln	Ile	Gly	Gly	Ser	Lys			115		120		Asp	Ile	Lys	Ser	Lys	Asn			130		135		Ile	Gly	Asp	Leu	Gly	Leu	145				150		Asp	Ile	Ile	Ala	Asn	Glu					165																																					
		115		120																																																																															
Asp	Ile	Lys	Ser	Lys	Asn			130		135		Ile	Gly	Asp	Leu	Gly	Leu	145				150		Asp	Ile	Ile	Ala	Asn	Glu					165																																																	
		130		135																																																																															
Ile	Gly	Asp	Leu	Gly	Leu	145				150		Asp	Ile	Ile	Ala	Asn	Glu					165																																																													
145				150																																																																															
Asp	Ile	Ile	Ala	Asn	Glu					165																																																																									
				165																																																																															

Ala Pro

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: MOUSE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

SEQ ID NO: 34
Mouse ActR-II

Met	Gly	Ala	Ala	Ala	Lys	Leu	Ala	Phe	Ala	Val	Phe	Leu	Ile	Ser	Cys
				5					10					15	
Ser	Ser	Gly	Ala	Ile	Leu	Gly	Arg	Ser	Glu	Thr	Gln	Glu	Cys	Leu	Phe
			20				25						30		
Phe	Asn	Ala	Asn	Trp	Glu	lys	Asp	Arg	Thr	Asn	Gln	Thr	Gly	Val	Glu
			35				40					45			
Pro	Cys	Tyr	Gly	Asp	Lys	Asp	Lys	Arg	Arg	His	Cys	Phe	Ala	Thr	Trp
			50			55					60				
Lys	Asn	Ile	Ser	Gly	Ser	Ile	Glu	Ile	Val	Lys	Gln	Gly	Cys	Trp	Leu
65					70				75					80	
Asp	Asp	Ile	Asn	Cys	Tyr	Asp	Arg	Thr	Asp	Cys	Val	Glu	Lys	Lys	Asp
			85					90					95		
Ser	Pro	Glu	Val	Tyr	Phe	Cys	Cys	Cys	Glu	Gly	Asn	Met	Cys	Asn	Glu
			100					105					110		
Lys	Phe	Ser	Tyr	Phe	Pro	Glu	Met	Glu	Val	Thr	Gln	Pro	Thr	Ser	Asn
			115				120					125			
Pro	Val	Thr	Pro	Lys	Pro	Pro	Tyr	Tyr	Asn	Ile	Leu	Leu	Tyr	Ser	Leu
			130				135				140				
Val	Pro	Leu	Met	Leu	Ile	Ala	Gly	Ile	Val	Ile	Cys	Ala	Phe	Trp	Val

145					150					155					160
Tyr	Arg	His	His	Lys	Met	Ala	Tyr	Pro	Pro	Val	Leu	Val	Pro	Thr	Gln
				165					170					175	
Asp	Pro	Gly	Pro	Pro	Pro	Pro	Ser	Pro	Leu	Leu	Gly	Leu	Lys	Pro	Leu
			180					185					190		
Gln	Leu	Leu	Glu	Val	Lys	Ala	Arg	Gly	Arg	Phe	Gly	Cys	Val	Trp	Lys
		195					200				205				
Ala	Gln	Leu	Leu	Asn	Glu	Tyr	Val	Ala	Val	Lys	Ile	Phe	Pro	Ile	Gln
	210					215				220					
Asp	Lys	Gln	Ser	Trp	Gln	Asn	Glu	Tyr	Glu	Val	Tyr	Ser	Leu	Pro	Gly
225					230				235					240	
Met	Lys	His	Glu	Asn	Ile	Leu	Gln	Phe	Ile	Gly	Ala	Glu	Lys	Arg	Gly
			245					250					255		
Thr	Ser	Val	Asp	Val	Asp	Leu	Trp	Leu	Ile	Thr	Ala	Phe	His	Glu	Lys
			260					265					270		
Gly	Ser	Leu	Ser	Asp	Phe	Leu	Lys	Ala	Asn	Val	Val	Ser	Trp	Asn	Glu
	275						280					285			
Leu	Cys	His	Ile	Ala	Glu	Thr	Met	Ala	Arg	Gly	Leu	Ala	Tyr	Leu	His
	290					295					300				
Glu	Asp	Ile	Pro	Gly	Leu	Lys	Asp	Gly	His	Lys	Pro	Ala	Ile	Ser	His
305					310				315					320	
Arg	Asp	Ile	Lys	Ser	Lys	Asn	Val	Leu	Leu	Lys	Asn	Asn	Leu	Thr	Ala
			325					330					335		
Cys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Leu	Lys	Phe	Glu	Ala	Gly	Lys	Ser
		340					345					350			
Ala	Gly	Asp	Thr	His	Gly	Gln	Val	Gly	Thr	Arg	Arg	Tyr	Met	Ala	Pro
	355					360						365			
Glu	Val	Leu	Glu	Gly	Ala	Ile	Asn	Phe	Gln	Arg	Asp	Ala	Phe	Leu	Arg
	370					375					380				
Ile	Asp	Met	Tyr	Ala	Met	Gly	Leu	Val	Leu	Trp	Glu	Leu	Ala	Ser	Arg
385					390				395					400	
Cys	Thr	Ala	Ala	Asp	Gly	Pro	Val	Asp	Glu	Tyr	Met	Leu	Pro	Phe	Glu
			405					410					415		
Glu	Glu	Ile	Gly	Gln	His	Pro	Ser	Leu	Glu	Asp	Met	Gln	Glu	Val	Val
		420						425				430			
Val	His	Lys	Lys	Lys	Arg	Pro	Val	Leu	Arg	Asp	Tyr	Trp	Gln	Lys	His
	435					440					445				
Ala	Gly	Met	Ala	Met	Leu	Cys	Glu	Thr	Ile	Glu	Glu	Cys	Trp	Asp	His
	450					455				460					
Asp	Ala	Glu	Ala	Arg	Leu	Ser	Ala	Gly	Cys	Val	Gly	Glu	Arg	Ile	Thr
465					470				475					480	
Gln	Met	Gln	Arg	Leu	Thr	Asn	Ile	Ile	Thr	Thr	Glu	Asp	Ile	Val	Thr
			485					490					495		
Val	Val	Thr	Met	Val	Thr	Asn	Val	Asp	Phe	Pro	Pro	Lys	Glu	Ser	Ser
			500				505					510			
Leu															

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 536 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: MOUSE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ACTR- IIB

Met	Thr	Ala	Pro	Trp	Ala	Ala	Leu	Ala	Leu	Leu	Trp	Gly	Ser	Leu	Cys	
			5						10					15		
Ala	Gly	Ser	Gly	Arg	Gly	Glu	Ala	Glu	Thr	Arg	Glu	Cys	Ile	Tyr	Tyr	
			20					25					30			
Asn	Ala	Asn	Trp	Glu	Leu	Glu	Arg	Thr	Asn	Gln	Ser	Gly	Leu	Glu	Arg	
		35					40					45				
Cys	Glu	Gly	Glu	Gln	Asp	Lys	Arg	Leu	His	Cys	Tyr	Ala	Ser	Trp	Arg	
	50					55					60					
Asn	Ser	Ser	Gly	Thr	Ile	Glu	Leu	Val	Lys	Lys	Gly	Cys	Trp	Leu	Asp	
65					70					75					80	
Asp	Phe	Asn	Cys	Tyr	Asp	Arg	Gln	Glu	Cys	Val	Ala	Thr	Glu	Glu	Asn	
				85					90					95		
Pro	Gln	Val	Tyr	Phe	Cys	Cys	Cys	Glu	Gly	Asn	Phe	Cys	Asn	Glu	Arg	
			100					105					110			
Phe	Thr	His	Leu	Pro	Glu	Pro	Gly	Gly	Pro	Glu	Val	Thr	Tyr	Glu	Pro	
		115					120						125			
Pro	Pro	Thr	Ala	Pro	Thr	Leu	Leu	Thr	Val	Leu	Ala	Tyr	Ser	Leu	Leu	
	130					135					140					
Pro	Ile	Gly	Gly	Leu	Ser	Leu	Ile	Val	Leu	Leu	Ala	Phe	Trp	Met	Tyr	
145					150					155					160	
Arg	His	Arg	Lys	Pro	Pro	Tyr	Gly	His	Val	Asp	Ile	His	Glu	Val	Arg	
				165					170					175		
Gln	Cys	Gln	Arg	Trp	Ala	Gly	Arg	Arg	Asp	Gly	Cys	Ala	Asp	Ser	Phe	
			180				185						190			
Lys	Pro	Leu	Pro	Phe	Gln	Asp	Pro	Gly	Pro	Pro	Pro	Pro	Ser	Pro	Leu	
		195					200					205				
Val	Gly	Leu	Lys	Pro	Leu	Gln	Leu	Leu	Glu	Ile	Lys	Ala	Arg	Gly	Arg	
	210					215					220					
Phe	Gly	Cys	Val	Trp	Lys	Ala	Gln	Leu	Met	Asn	Asp	Phe	Val	Ala	Val	
225					230					235					240	
Lys	Ile	Phe	Pro	Leu	Gln	Asp	Lys	Gln	Ser	Trp	Gln	Ser	Glu	Arg	Glu	
				245					250					255		
Ile	Phe	Ser	Thr	Pro	Gly	Met	Lys	His	Glu	Asn	Leu	Leu	Gln	Phe	Ile	
			260					265						270		
Ala	Ala	Glu	Lys	Arg	Gly	Ser	Asn	Leu	Glu	Val	Glu	Leu	Trp	Leu	Ile	
		275					280						285			
Thr	Ala	Phe	His	Asp	Lys	Gly	Ser	Leu	Thr	Asp	Tyr	Leu	Lys	Gly	Asn	
	290					295					300					
Ile	Ile	Thr	Trp	Asn	Glu	Leu	Cys	His	Val	Ala	Glu	Thr	Met	Ser	Arg	
305					310					315					320	
Gly	Leu	Ser	Tyr	Leu	His	Glu	Asp	Val	Pro	Trp	Cys	Arg	Gly	Glu	Gly	
				325					330					335		
His	Lys	Pro	Ser	Ile	Ala	His	Arg	Asp	Phe	Lys	Ser	Lys	Asn	Val	Leu	
			340					345						350		

Leu	Lys	Ser	Asp	Leu	Thr	Ala	Val	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Val
		355					360					365			
Arg	Phe	Glu	Pro	Gly	Lys	Pro	Pro	Gly	Asp	Thr	His	Gly	Gln	Val	Gly
	370					375					380				
Thr	Arg	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Glu	Gly	Ala	Ile	Asn	Phe
385					390					395					400
Gln	Arg	Asp	Ala	Phe	Leu	Arg	Ile	Asp	Met	Tyr	Ala	Met	Gly	Leu	Val
			405						410					415	
Leu	Trp	Glu	Leu	Val	Ser	Arg	Cys	Lys	Ala	Ala	Asp	Gly	Pro	Val	Asp
		420						425					430		
Glu	Tyr	Met	Leu	Pro	Phe	Glu	Glu	Glu	Ile	Gly	Gln	His	Pro	Ser	Leu
	435						440					445			
Glu	Glu	Leu	Gln	Glu	Val	Val	Val	His	Lys	Lys	Met	Arg	Pro	Thr	Ile
	450					455					460				
Lys	Asp	His	Trp	Leu	Lys	His	Pro	Gly	Leu	Ala	Gln	Leu	Cys	Val	Thr
465					470					475					480
Ile	Glu	Glu	Cys	Trp	Asp	His	Asp	Ala	Glu	Ala	Arg	Leu	Ser	Ala	Gly
			485					490						495	
Cys	Val	Glu	Glu	Arg	Val	Ser	Leu	Ile	Arg	Arg	Ser	Val	Asn	Gly	Thr
		500					505						510		
Thr	Ser	Asp	Cys	Leu	Val	Ser	Leu	Val	Thr	Ser	Val	Thr	Asn	Val	Asp
	515					520						525			
Leu	Leu	Pro	Lys	Glu	Ser	Ser	Ile								
	530					535									

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Met	Gly	Arg	Gly	Leu	Leu	Arg	Gly	Leu	Trp	Pro	Leu	His	Ile	Val	Leu
				5					10					15	
Trp	Thr	Arg	Ile	Ala	Ser	Thr	Ile	Pro	Pro	His	Val	Gln	Lys	Ser	Val
		20					25						30		
Asn	Asn	Asp	Met	Ile	Val	Thr	Asp	Asn	Asn	Gly	Ala	Val	Lys	Phe	Pro
	35					40					45				
Gln	Leu	Cys	Lys	Phe	Cys	Asp	Val	Arg	Phe	Ser	Thr	Cys	Asp	Asn	Gln
	50				55					60					
Lys	Ser	Cys	Met	Ser	Asn	Cys	Ser	Ile	Thr	Ser	Ile	Cys	Glu	Lys	Pro
65					70				75					80	
Gln	Glu	Val	Cys	Val	Ala	Val	Trp	Arg	Lys	Asn	Asp	Glu	Asn	Ile	Thr
		85					90						95		
Leu	Glu	Thr	Val	Cys	His	Asp	Pro	Lys	Leu	Pro	Tyr	His	Asp	Phe	Ile
	100						105					110			
Leu	Glu	Asp	Ala	Ala	Ser	Pro	Lys	Cys	Ile	Met	Lys	Glu	Lys	Lys	Lys

		115					120					125				
Pro	Gly	Glu	Thr	Phe	Phe	Met	Cys	Ser	Cys	Ser	Ser	Asp	Glu	Cys	Asn	
	130					135					140					
Asp	Asn	Ile	Ile	Phe	Ser	Glu	Glu	Tyr	Asn	Thr	Ser	Asn	Pro	Asp	Leu	
145					150					155					160	
Leu	Leu	Val	Ile	Phe	Gln	Val	Thr	Gly	Ile	Ser	Leu	Leu	Pro	Pro	Leu	
				165					170					175		
Gly	Val	Ala	Ile	Ser	Val	Ile	Ile	Ile	Phe	Tyr	Cys	Tyr	Arg	Val	Asn	
			180					185					190			
Arg	Gln	Gln	Lys	Leu	Ser	Ser	Thr	Trp	Glu	Thr	Gly	Lys	Thr	Arg	Lys	
		195					200					205				
Leu	Met	Glu	Phe	Ser	Glu	His	Cys	Ala	Ile	Ile	Leu	Glu	Asp	Asp	Arg	
	210					215					220					
Ser	Asp	Ile	Ser	Ser	Thr	Cys	Ala	Asn	Asn	Ile	Asn	His	Asn	Thr	Glu	
225					230					235					240	
Leu	Leu	Pro	Ile	Glu	Leu	Asp	Thr	Leu	Val	Gly	Lys	Gly	Arg	Phe	Ala	
				245					250					255		
Glu	Val	Tyr	Lys	Ala	Lys	Leu	Lys	Gln	Asn	Thr	Ser	Glu	Gln	Phe	Glu	
			260					265					270			
Thr	Val	Ala	Val	Lys	Ile	Phe	Pro	Tyr	Glu	Glu	Tyr	Ala	Ser	Trp	Lys	
		275					280					285				
Thr	Glu	Lys	Asp	Ile	Phe	Ser	Asp	Ile	Asn	Leu	Lys	His	Glu	Asn	Ile	
	290					295					300					
Leu	Gln	Phe	Leu	Thr	Ala	Glu	Glu	Arg	Lys	Thr	Glu	Leu	Gly	Lys	Gln	
305					310					315					320	
Tyr	Trp	Leu	Ile	Thr	Ala	Phe	His	Ala	Lys	Gly	Asn	Leu	Gln	Glu	Tyr	
				325					330					335		
Leu	Thr	Arg	His	Val	Ile	Ser	Trp	Glu	Asp	Leu	Arg	Lys	Leu	Gly	Ser	
			340					345					350			
Ser	Leu	Ala	Arg	Gly	Ile	Ala	His	Leu	His	Ser	Asp	His	Thr	Pro	Cys	
		355					360					365				
Gly	Arg	Pro	Lys	Met	Pro	Ile	Val	His	Arg	Asp	Leu	Lys	Ser	Ser	Asn	
	370					375					380					
Ile	Leu	Val	Lys	Asn	Asp	Leu	Thr	Cys	Cys	Leu	Cys	Asp	Phe	Gly	Leu	
385					390					395					400	
Ser	Leu	Arg	Leu	Asp	Pro	Thr	Leu	Ser	Val	Asp	Asp	Leu	Ala	Asn	Ser	
				405					410					415		
Gly	Gln	Val	Gly	Thr	Ala	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Glu	Ser	
			420					425					430			
Arg	Met	Asn	Leu	Glu	Asn	Ala	Glu	Ser	Phe	Lys	Gln	Thr	Asp	Val	Tyr	
		435					440					445				
Ser	Met	Ala	Leu	Val	Leu	Trp	Glu	Met	Thr	Ser	Arg	Cys	Asn	Ala	Val	
	450					455					460					
Gly	Glu	Val	Lys	Asp	Tyr	Glu	Pro	Pro	Phe	Gly	Ser	Lys	Val	Arg	Glu	
465					470					47						

545 550 555 560
Gly Ser Leu Asn Thr Thr Lys
 565

SEQ ID NO: 37
C. elegans Daf-1:

Pro	Gly	Ile	Met	Pro	Asn	Asn	Met	Lys	Asp	Met	Leu	Asp	Val	Leu	Glu	260	265	270
Glu	Thr	Ser	Gly	Ser	Gly	Met	Gly	Pro	Thr	Thr	Leu	His	Lys	Leu	Thr	275	280	285
Ile	Gly	Gly	Gln	Ile	Arg	Leu	Thr	Gly	Arg	Val	Gly	Ser	Gly	Arg	Phe	290	295	300
Gly	Asn	Val	Ser	Arg	Gly	Asp	Tyr	Arg	Gly	Glu	Ala	Val	Ala	Val	Lys	305	310	315
Val	Phe	Asn	Ala	Leu	Asp	Glu	Pro	Ala	Phe	His	Lys	Glu	Thr	Glu	Ile	325	330	335
Phe	Glu	Thr	Arg	Met	Leu	Arg	His	Pro	Asn	Val	Leu	Arg	Tyr	Ile	Gly	340	345	350
Ser	Asp	Arg	Val	Asp	Thr	Gly	Phe	Val	Thr	Glu	Leu	Trp	Leu	Val	Thr	355	360	365
Glu	Tyr	His	Pro	Ser	Gly	Ser	Leu	His	Asp	Phe	Leu	Leu	Glu	Asn	Thr	370	375	380
Val	Asn	Ile	Glu	Thr	Tyr	Tyr	Asn	Leu	Met	Arg	Ser	Thr	Ala	Ser	Gly	385	390	395
Leu	Ala	Phe	Leu	His	Asn	Gln	Ile	Gly	Gly	Ser	Lys	Glu	Ser	Asn	Lys	405	410	415
Pro	Ala	Met	Ala	His	Arg	Asp	Ile	Lys	Ser	Lys	Asn	Ile	Met	Val	Lys	420	425	430
Asn	Asp	Leu	Thr	Cys	Ala	Ile	Gly	Asp	Leu	Gly	Leu	Ser	Leu	Ser	Lys	435	440	445
Pro	Glu	Asp	Ala	Ala	Ser	Asp	Ile	Ile	Ala	Asn	Glu	Asn	Tyr	Lys	Cys	450	455	460
Gly	Thr	Val	Arg	Tyr	Leu	Ala	Pro	Glu	Ile	Leu	Asn	Ser	Thr	Met	Gln	465	470	475
Phe	Thr	Val	Phe	Glu	Ser	Tyr	Gln	Cys	Ala	Asp	Val	Tyr	Ser	Phe	Ser	485	490	495
Leu	Val	Met	Trp	Glu	Thr	Leu	Cys	Arg	Cys	Glu	Asp	Gly	Asp	Val	Leu	500	505	510
Pro	Arg	Glu	Ala	Ala	Thr	Val	Ile	Pro	Tyr	Ile	Glu	Trp	Thr	Asp	Arg	515	520	525
Asp	Pro	Gln	Asp	Ala	Gln	Met	Phe	Asp	Val	Val	Cys	Thr	Arg	Arg	Leu	530	535	540
Arg	Pro	Thr	Glu	Asn	Pro	Leu	Trp	Lys	Asp	His	Pro	Glu	Met	Lys	His	545	550	555
Ile	Met	Glu	Ile	Ile	Lys	Thr	Cys	Trp	Asn	Gly	Asn	Pro	Ser	Ala	Arg	565	570	575
Phe	Thr	Ser	Tyr	Ile	Cys	Arg	Lys	Arg	Met	Asp	Glu	Arg	Gln	Gln	Leu	580	585	590
Leu	Leu	Asp	Lys	Lys	Ala	Lys	Ala	Val	Ala	Gln	Thr	Ala	Gly	Val	Thr	595	600	605
Val	Gln	Asp	Arg	Lys	Ile	Leu	Gly	Pro	Gln	Lys	Pro	Lys	Asp	Glu	Ser	610	615	620
Pro	Ala	Asn	Gly	Ala	Pro	Arg	Ile	Val	Gln	Lys	Glu	Ile	Asp	Arg	Glu	625	630	635
Asp	Glu	Gln	Glu	Asn	Trp	Arg	Glu	Thr	Ala	Lys	Thr	Pro	Asn	Gly	His	645	650	655
Ile	Ser	Ser	Asn	Asp	Asp	Ser	Ser	Arg	Pro	Leu	Leu	Gly				660	665	

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Asp Leu Lys Pro Glu Asn

5

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Asp Leu Ala Ala Arg Asn

5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Asp Ile Lys Ser Lys Asn

5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Asp Phe Lys Ser Lys Asn

5

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Asp Leu Lys Ser Ser Asn

5

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (D) OTHER INFORMATION: First Xaa is Thr or Ser;
fourth Xaa is Tyr or Phe; Each other Xaa
may be any amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Gly Xaa Xaa Xaa Xaa Xaa

5

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (D) OTHER INFORMATION: First Xaa is any amino acid;
second Xaa is Ile or Val;
third Xaa is Lys or Arg;
fourth Xaa is Thr or Met.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Xaa Pro Xaa Xaa Trp Xaa

5

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Gly Thr Arg Arg Tyr Met

5

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Gly Thr Ala Arg Tyr Met

5